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GenCore version 5.1.6
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                 Copyright
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- protein search, using sw model OM protein

September Run on:

5, 2004, 09:47:29; Search time 6.90909 Seconds (without alignments) 125.302 Million cell updates/sec

US-09-761-636A-10 50 1 CSVPLTSVC 9 score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

seq length: 0 seq length: 2000000000 DB DB Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	S48719	AD0990	CB6015	S47693	C91169	F64484	B55538	S54788	T29764	D97130	A37931	S65447	NWR P1	865478	S65481	S65482	S65480	T34649	PS0426	NWRP2	807828	A25997	825137	825130	S25134	810018	\$52025	YRNC	835592
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	Score	43	41	41	41	41	39	38	36	36	35	35	35	35	35	35	35	32	35	35	35	35	35	35	35	35	35	35	35	34
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ADH2 dehydrogenas	n nanB - rane	ptical	NADH2 dehvdrogenas	12 dehydrogenas	12 dehydrogenas	2 dehydrogenas	2 dehydrogenes	TVDOThetical trans	exprolusaccharide	prostackolin recen	process receptors for the process of	overtherical prote	arginine tPNA 1400	arginine-tRNA liga	ypothetical prote
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T12116	S15382	B96583	T11729	T11687	T11702	T11697	T11731	S70841	577634	A57066	E71716	T08794	JC4365	JN0870	T17122
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141	178	192	265	270	273	277	278	376	377	386	418	565	629	661	699
68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0
34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

phospholipase-A(2) receptor protein - mouse (5.Species: Mus musculus (house mouse) (5.Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Jun-2000 (5.Accession: 848719 B.Higashino, K.; Ishizaki, J.; Kishino, J.; Ohara, O.; Arita, H. B.Higashino, K.; Ishizaki, J.; Kishino, J.; Ohara, O.; Arita, H. A.Fitle: Structural Comparison of phospholipase-A(2)-binding regions in phospholipase-A A.Reference number: 848719 A.Referens: preliminary A.Molecule type: mRNA A.Residues: 1-1487 cHIG>

A,Cross-references: GB:D30779, NID:g1375042; PIDN:BAA06443.1; PID:g691754 C;Superfamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II F;181-222/Domain: fibronectin type II repeat homology <2F1> F;380-503/Domain: C-type lectin homology <LCH>

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Gaps .; 0 2; Length 1487; Query Match

86.0%; Score 43; DB

Best Local Similarity 77.8%; Pred. No. 8;

Matches 7; Conservative 1; Mismatches

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929 CSVPLPSIC 937 1 CSVPLTSVC 9 g ð

probable membrane protein STY4229 [imported] - Salmonella enterica subsp. enterica serowary philosocias alamonella enterica subsp. enterica serowary philosocias alamonella enterica subsp. enterica serowary philosocias alamonella enterica serowary philosocias alamonella enterica serowary philosocias alamonella enterica serowary serowary serowary serowary serosia possible sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002 C.Accession. AD0990

R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Tite: Complete genome sequence of a multiple drug resistant Salmonella enterica serow A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Returus: preliminary
A;Molecule type: DNA
A;Residues: 1-349 c-PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08048.1; PID:g16505028; GSPDB:GN00176
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:

Query Match

82.0%; Score 41; DB 2; Length 349;

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Appethetical protein BC64323 [imported] - Escherichia coli (strain O157:H7, substrain R hypothetical protein BC64323 [imported] - Escherichia coli (strain O157:H7, substrain R c; Baceise: Escherichia coli (c; Bate: 18-Ju1-2001 #sequence_revision 18-Ju1-2001 #text_change 03-Aug-2001 C; Accession: C9169
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res: 8, 11-22, 2001 A; Itle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen, A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: C91169
A; Residues: 1-376 cHAX>
A; Residues: 1-376 cHAX>
A; Residues: 1-376 cHAX>
A; Residues: 1-376 cHAX>
A; Cross-references: GB:BNA00007; PIDN:BAB37746.1; PID:g13363797; GSPDB:GN00154
A; Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable transaminase (EC 2.6.1.-) MJ479 [similarity] - Methanococcus jannaschii probable transaminase (EC 2.6.1.-) MJ479 [similarity] - Methanococcus jannaschii C;Species: Ja:Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jun-2000 C;Accession: F64484 R: Kirkness, B.F.; Meinstock, K.G.; Merrick, J.M.; Glodek, A;Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Meinstock, K.G.; Merrick, J.M.; Glodek, A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Atitle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi A;Reference number: A6430; MUID:96337999; PMID:8688087 A;Accession: F64484 A;Residues: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1432 ABUL> A;Residues: 1432 ABUL> A;Residues: J432 ABUL> A;Residues: GB:U67588; GB:L77117; NID:g1592111; PID:g1592118; TIGR:MJ479; PID
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BS5538
C. Protein - Pseudomonas syringae pv. syringae (strain B728a) (fragment)
C. Species: Pseudomonas syringae pv. syringae
C. Species: Pseudomonas syringae pv. syringae
C. Date: 08-Sep-1995 #sequence_revision 08-Sep-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.0%; Score 41; DB 2; Length 376; 100.0%; Pred. No. 5.3; ive 0; Mismatches 0; Indels
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C,Superfamily: conserved hypothetical protein HI0338
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C, Superfamily: aspartate transaminase
C, Keywords: aminotransferase
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                  341 SVPLTSVC 348
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SVPLTSVC 9
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submitted to the EMBL Data Library, March 1994

A; Reference number: 84766

A; Reference number: 84766

A; Recession: 84763

A; Status: preliminary

A; Molecule type: DNA

A; Readules: 1-376 < PLD.

A; Readules: 1-376 < PLD.

A; Rose, D.J.; Mau, B.; Shao, Y.

A; Rose, D.J.; Mau, B.; Shao, Y.

A; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Rile: The complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUID:97426617; PMID:9278503

A; Reference number: B65144

A; Retus: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-376 < BLAT>

A; Residues: 1-376 < BLAT>

A; Experimental source: strain K-12, substrain MG1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Accession: C86015
A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Rolecule type: DNA
A, Rolecule type: DNA
A, Residues: 1-364 <8T0>
A, Residues: 1-364 <8T0>
A, Experimental source: strain O157:H7, substrain EDL933
A, Experimental source: strain O157:H7, substrain EDL933
C, Genetics:
A, Genetics:
A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genet
                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein yhhT [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Accession: C86015
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, S29-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 8; Conservative 0; Mismatches 0; Indels
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A;Gene: yhbT
A;Start codon: GTG
C;Superfamily: conserved hypothetical protein HI0338
            Pred. No. 4.9; Mismatches
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                     100.0%;
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Best Local Similarity 100.
Matches 8; Conservative
                                                            Conservative
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                     Best Local Similarity
Matches 8; Conserv
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C;Species: Clostridium acetoburylium (C) and (C) and (C) are constructed acetoburylium acetoburylium (C) and (C) are constructed acetoburylium acetoburylium (C) acession: D97130 (C) accession: D9713
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C;Date: 31.May-1991 #sequence_revision 31-May-1991 #text_change 12-Apr-1995
C;Accession: A37931
R;Svendsen, I.; Nicolova, D.; Goshev, I.; Genov, N.
Carlsbherg Res. Commun. 54, 231-239, 1989
A;Title: Isolation and characterization of a trypsin inhibitor from the seeds of kohlrab A;Reference number: A37931; MUID:91282906; PMID:2490369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription regulator (phage-related) (Xre. family) [imported] - Clostridium acetobutyl
                                                                              2073/1; 2098/2; 2146/3
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A;Accession: D97130
A;Status: prefilminary
A;Molecule type: DNA
A;Residues: 1-91 <KUR>
A;Coss-references: GB:AE001437; PIDN:AAK79831.1; PID:g15024845; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                       A;Introns: 400/2; 1608/3; 1644/1; 1674/3; 1666/2; 1731/2; 2073/1; 2098/2; C;Superfamily: LDL receptor ligand-binding repeat homology C;Superfamily: LDL receptor ligand-binding repeat homology LDLL> F;51-85/Domain: LDL receptor ligand-binding repeat homology LDLL> F;50-132/Domain: LDL receptor ligand-binding repeat homology LDLL> F;90-132/Domain: LDL receptor ligand-binding repeat homology LDLL> F;190-25/Domain: LDL receptor ligand-binding repeat homology LDLL> F;280-272/Domain: LDL receptor ligand-binding repeat homology LDLL> F;285-272/Domain: LDL receptor ligand-binding repeat homology LDLL> F;285-378/Domain: LDL receptor ligand-binding repeat homology LDLL> F;286-405/Domain: LDL receptor ligand-binding repeat homology LDLL> F;861-903/Domain: LDL receptor ligand-binding repeat homology LDLL> F;861-903/Domain: LDL receptor ligand-binding repeat homology LDLL> F;861-903/Domain: LDL receptor ligand-binding repeat homology LDLL> F;993-1027/Domain: LDL receptor ligand-binding repeat homology LDLL> F;993-1027/Domain: LDL receptor ligand-binding repeat homology LDLL> F;913-1063/Domain: LDL receptor ligand-binding repeat homology LDLL> F;913-1027/Domain: LDL receptor ligand-binding repeat homology LDLL> F;913-1027/Domain: LDL receptor ligand-binding repeat homology LDLL> F;913-1027/Domain: LDL receptor ligand-binding repeat homology LDLL> F;1031-1063/Domain: LDL receptor ligand-binding repeat homolo
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Pred. No. 2.2e+02;
1; Mismatches 0; Indels
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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54 CSIGYTSVC 62
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922 IPLTSVC 928
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Matches 6; Conserv
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-591 < SID.
A;Residues: 1-591 < SID.
C;Superferences: EmBL: 249233; NID: 9806541; PIDN: CRA89202.1; PID: g806542
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase; calmodulin repeat homology calcium-dinase arp-binding motif
C;Accession: B55538
R;Rich, J.J.; Kinscherf, T.G.; Kitten, T.; Willis, D.K.
Dacteriol. 176, 74684-7475, 1994
A;Title: Genetic evidence that the gacA gene encodes the cognate response regulator for A;Reference number: A55538; WIID:95095914; PMID:8002569
A;Accession: B5538
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <RIC>
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A;Experimental source: strain Bristol N2; clone T21E3
C;Genetics:
A;Gene: CESP:T21E3.3
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SS4788
Calcium-stimulated protein kinase - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Species: Unlamydomonas eugametos
C;Bate: 08-501-11995 #sequence_revision 21-Jul-1995 #text_change 18-Jun-1999
R;Siderius, M.H.
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C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C; Accession: T29764
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A;Description: Cloning a CDPK from Chlamydomonas eugametos.
A;Reference number: S54788
A;Accession: S54788
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R;Du, Z.; Le, T.T.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid T21E3.
A;Reference number: Z20681
A;Accession: T29764
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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F,489-521/Domain: calmodulin repeat homology <EF2>
F,526-557/Domain: calmodulin repeat homology <EF3>
F,559-591/Domain: calmodulin repeat homology <EF3>
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Pred. No.
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66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
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C, Genetics:
A, Gene: uvrC
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13 CSVPASTVC 21
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Best Local Similarity
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solution Sin a I (clone SINS) - white mustard (fragment)
C;Species: Sinapis alba (white mustard)
C;Species: Sinapis alba (white mustard)
C;Species: Sal-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: 656478
R;Gonzalez de la Pena, M.A.; Monsalve, R.I.; Batanero, B.; Villalba, M.; Rodriguez, R. B;Gonzalez de la Pena, M.A.; Monsalve, R.I.; Batanero, B.; Villalba, M.; Rodriguez, R. A;Title: Expression in Escherichia coli of Sin a 1, the major allergen from mustard.
A;Reference number: 85447; MUD: 96235251; PMID: 8647131
A;Reference number: 865478
A;Residues: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-145 <GONS
C;Genetics:
A;Genetics:
A;Genetics
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C;Species: Sinapis alba (white mustard)
C;Species: Sinapis alba (white mustard)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: 565481
R;Gonzalez de la Pena, M.A.; Monsalve, R.I.; Batanero, E.; Villalba, M.; Rodriguez, R. Biochem: 237, 827-832, 1996
A;Title: Expression in Escherichia coli of Sin a 1, the major allergen from mustard. A;Reference number: 865447; MUID:96235251; PMID:8647131
A;Accession: 865481
A;Accession: 865481
A;Resione ruppe: DNA
A;Resiones: 1-145 <GON>
A;Resiones: 1-145 <GON>
A;Resiones: EMBL:X91801; NID:g1009437; PIDN:CAA62911.1; PID:g1009438
C;Genetics:
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Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: sin3
C,Superfamily: wheat alpha-amylase
C,Keywords: seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.0%;
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Best Local Similarity 55.b.
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Best Local Similarity 55.6
Matches 5; Conservative
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127 CNIPQVSVC 135
114 CNIPQVSVC 122
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Blochen. 177, 159-166, 1988
A;Title: Primary structure of the major allergen of yellow mustard (Sinapis alba L.) see
A;Reference number: S01791; MUID:89030681; PMID:3181153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: A01330
R;Crouch, M.L.; Tenbarge, K.M.; Simon, A.B.; Ferl, R.
J. Mol. Appl. Genet. 2, 273-283, 1983
A;Title: CDNA clones for Brassica napus seed storage proteins: evidence from nucleotide A;Reference number: A92836; MUID:84113267; PMID:6689334
A;Accession: A01330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allergen Sin a I - white mustard

N.Alternate names: allergen Sin a I large chain

C.Species: Sinapis alba (white mustard)

C.Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C.Accession: 865447; 801792

R.Gonzalez de la Pena, M.A.; Monsalve, R.I.; Batanero, E.; Villalba, M.; Rodriguez, Bur. J. Biochem. 237, 827-832, 1996

A.Title: Expression in Bscherichia coli of Sin a 1, the major allergen from mustard. A.Reference number: 865447; MUID:96235251; PMID:8647131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
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NyAlternate names: 1.7S seed storage protein
C.Species: Brassica napus (rape)
C.Species: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 18-Jun-1999
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A; Residues: 1-133 <CRO.
A; Cross-references: GB: KO1544; NID: g167174; PIDN: AAA33005.1; PID: g167175
A; Experimental Bource: cv. Tower
C; Superfamily: wheat alpha-amylase inhibitor
C; Superfamily: wheat lapha-amylase inhibitor
F; Keywords: seed; storage protein
F; 1-30/Product: napin 1 small chain (fragment) #status predicted <SCH>F; 50-130/Product: napin 1 large chain #status predicted <LCH>
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                                                                                                            Length 124;
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                                                                                                        70.0%; Score 35; DB ilarity 55.6%; Pred. No. 24; Conservative 2; Mismatches
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A,Molecule type: protein
A,Residues: 40-127 <MEN>
C,Superfamily: wheat alpha-amylase inhibitor
C,Keywords: seed; storage protein
   A,Residues: 1-124 <SVE>
C,Superfamily: wheat alpha-amylase inhibitor
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Matches 5; Conservative
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A,Residues: 1-127 <GON>
A,Experimental source: seed
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109 CNIPQVSVC 117
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

September 5, 2004, 09:38:39; Search time 4.09091 Seconds (without alignments) 114.554 Million cell updates/sec Run on:

US-09-761-636A-10 50 1 CSVPLTSVC 9

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	937622 escherichia Q52377 pseudomonas P1532 sinapis alb P01090 brassica na P01090 brassica na Q91033 brassica na Q91031 massica na Q9401 mas musculu P80207 brassica na Q45407 ralstonia s P43119 homo sapien Q9116 rattus norv P54136 homo sapien Q91744 neisseria m Q91744 neisseria m Q950774 rickettsia Q92174 rickettsia Q92174 rickettsia Q92174 rickettsia Q92174 saccharomyc P53071 saccharomyc P53071 saccharomyc P53071 saccharomyc P56718 homo sapien Q96941 homo sapien Q95251 rattus norv Q96941 homo sapien Q974X1 candidatus Q9315 homo sapien Q73915 homo sapien Q43915 homo sapien Q43915 homo sapien Q43915 homo sapien Q43915 homo sapien Q6550 oryctolagus P6550 oryctolagus
SUMMARIES	YHHT BCOLI UVRC_BESY ALLI SINAL 2SSI_BRANA 2SS2_BRANA 2SS2_BRANA 2SS3_BRANA 2SS3_BRANA 2SS3_BRANA 2SS3_BRANA 2SSB_BRANA 2
Length DB	10.00   10.00
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Score	  -  - 
Result No.	1144777 8 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Q9h1b4 homo sapien	092180 bos tauris	O9bvv6 homo gapien	P12859 pisum sativ	0887pg pseudomonas	048965 mycopiasma	079422 branchiosto	043310 homo sanien	047430 branchiosto	P58797 coturnix co	P18547 porcine par
NXF5_HUMAN	GENT BOVIN	RN29 HUMAN	G3PB_PEA	ALG8 PSESM	PYRG_MYCCA	NU5M BRALA	Y427 HUMAN	NU5M BRAFL	NXF1 COLUA	VNCS_PAVPN
4		Н	Н	-	Н	7	н	٦	٦	н .
397	427	436	451	493	502	598	598	599	616	099
64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0
32	32	32	32	32	32	32	32	32	32	32
8. 6. 4. 7.	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1  THE ECOLI STANDARD, PRT; 349 AA.  By 197622, 796700, 087629;  DT 01-NOV-1997 (Rel. 30, Created)  DT 01-NOV-1997 (Rel. 30, Leated)  DT 01-NOV-1997 (Rel. 30, Leated)  DT 28-PEB-2003 (Rel. 41, Last annotation update)  DT 28-PEB-2003 (Rel. 41, Last annotation update)  DY 38-PEB-2003 (Rel. 41, Last annotation update)  DY 38-PEB-2003 (Rel. 41, Last annotation update)  DY 38-PEB-2003 (Rel. 41, Last annotation update)  DY MHT OR B344 OR Z4484 OR ECS4323.  DESCHERCHIA COLI 017:HJ.  DESCHERCHIA COLI 017:HJ.  RESCHERCE FROM N.A.  NULL TAXID-562, 83334;  RN MEDLIES-9418600; PubMedeB041820;  RN MEDLIES-1017-147 (ED1933 / APCC 700927;  RN MEDLIES-21074935; PubMed-211206551949.  RN MEDLIES-21074935; PubMed-2112065994.  RN MEDLIES-21074935; PubMed-21120659952;  RN MEDLIES-21074935; PubMed-2112069952;  RN MEDLIES-21074938; NA W. M. M. A. M. M. M. A. M. A. M.
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Gaps

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Indels

76.0%; Score 38; DB 1; Length 150; 66.7%; Pred. No. 1.5;

2; Mismatches

16999 MW; ACC38718B5F1E2B1 CRC64;

150

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PROSITE; PS50164; UVRC_1; 1.
SOS response; Excision nuclease; DNA repair; DNA recombination;
                                                                       SMART; SM00465; GIYC; 1.
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CSVPASTVC 21
                                                                                                                               1 CSVPLTSVC 9
                                                         SEQUENCE 150 AA;
                                     excision.
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Rich J.J., Kinschef T.G., Kitten T., Willis D.K.;
Wienelic evidence that T.G., Kitten T., Willis D.K.;
Genetic evidence that T.G., Kitten T., Willis D.K.;
regulator for the lemA sensor in Pseudomonas syringae.";
J. Bacteriol. 176:7468-7475(1994).
J. Bacteriol. 176:7468-7475(1994).
FUNCTION: The UVARB. repair system catalyzes the recognition and processing of DNA lesions. UvrC both incises the 5' and 3' sides of the lesion. The N-terminal half is responsible for the 3' incision and the C-terminal half is responsible for the 5' incision (By similarity).
-!- SUBUNIT: Interacts with uvrB in an incision complex (By
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UVRABC system protein C (UvrC protein) (Excinuclease ABC subunit C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                        ٥:
                                                                                                                                                                                                                               Length 349;
                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1. SUBGELLULAR LOCATION: Cytoplasmic (By similarity). -1. SIMILARITY: Belongs to the uvrC family.
                                                                                                    Complete proteome.
                                                                                                                                                                                                           275ADBAD4FD58257 CRC64;
                                                                                                                                                                                                                                 DB 1;
0.95;
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                                                                                                                                                                                                                                   Score 41;
Pred. No.
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                EMBL; U00039; AAB18449.1, ALT INIT.
EMBL; AE000423; AAC76499.1, ALT INIT.
EMBL; AE005570; AAG58583.1; ALT INIT.
EMBL; AP002565; BAB37746.1; ALT_INIT.
                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95095914; PubMed=8002569;
                                                                                                                                                                                                                                    82.0°,
100.0%; Pre
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InterPro; IPR000305; UvrC N.
Pfam; PF01541; Exci_endo_N; 1.
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15-JUL-1998 (Rel. 36, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                            38522 MW;
                                                                        InterPro; IPR002549; UPP0118.
Pfam; PP01594; UPP0118; 1.
Hypothetical protein; Transmen
TRANSMEM 11
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                                                                                                                                                                                                                                   82.0%;
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                                                                 EcoGene; EG12220; yhhT
                                                                                                                                                                                                                                                                                                           314 SVPLTSVC 321
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209
235
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293
349 AA;
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STRAIN=B728a;
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Q52377;
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                                                                                                                                                                                                                                                                                                      Menendez-Arias L., Moneo I., Dominguez J., Rodriguez R.;
"Primary structure of the major allergen of yellow mustard (Sinapis alba L.) seed, Sin a I.";
Eur. J. Biochem. 177:159-166(1988).
-!- FUNCTION: This is a 2S seed storage protein.
-: SUBUNIT: The protein consists of two chains linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- ALLERGEN: Causes an allergic reaction in human. Causes cabbage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LARGE CHAIN.
R -> G.
7 4CD920284F04EEFD CRC64;
                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Allergen Sin a 1, small and large chains (Sin a I).
Sinapis alba (White mustard) (Brassica hirta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 AA
127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; irrucuca, prints; PR00496; NAPIN.
ProDom; PD002498; Napin; 1.
SMART; SM0499; AAI; 1.
Allergen; Seed storage protein.
39 SMALL CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35;
Pred. No. 5
                                                                                                                                                                                                                                                                            TISSUE=Seed;
MEDLINE=89030681; PubMed=3181153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14180 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S01791; S01791.
PIR; S65447; S65447.
InterPro; IPR003612; AAI.
InterPro; IPR000617; Napin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 55.6
Les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986
21-JUL-1986
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2551 BRANA
P01091;
  ALL1 SINAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                         from a precursor polypeptide.";
J. Mol. Appl. Genet. 2:273-283(1983).
-!- FUNCTION: The small, basic, water-soluble napins are one of the two major kinds of storage proteins synthesized in the seed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: The mature protein consists of a small and a large chain linked by disulfide bonds.
-!- TISSUE SPECIFICITY: Cotyledons and the axis.
-!- SIMILARITY: Belongs to the 2S seed storage albumins family.
                                                                                                                                                                                                                                                                                                                                                                            Crouch M.L., Tenbarge K.M., Simon A.B., Ferl R.; "cDNA clones for Brassica napus seed storage proteins: evidence from nucleotide sequence analysis that both subunits of napin are cleaved
                                                                                                                                                                         MEDLINE-87033665; PubMed-3771543;
Ericson M.L., Roedin J., Lenman M., Glimelius K., Josefsson L.-G.,
                                                                                                                                                                                                                                "Structure of the rapeseed 1.7 S storage protein, napin, and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.0%; Score 35; DB 1; Length 178; 55.6%; Pred. No. 7.2;
                                                                                        Josefsson L.-G.;
Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D -> N (IN REF. 4).
S -> N (IN REF. 4).
734E561971B539FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMALL CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LARGE CHAIN.
                               Biol. Chem. 262:12196-12201(1987).
                                                                                                                                                                                                                                                                          Biol. Chem. 261:14576-14581(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Tower;
MEDLINE=84113267; PubMed=6689334;
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PIR; A29801; A25997.
InterPro; IPR003612; AAI.
InterPro; IPR000617; Napin.
Pfam; PF00234; Lryp, alpha_amyl; 1.
PRINTS; PR00496; NAPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38
74 SN
175
175 LL
76
20104 MW;
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EMBL; J02586; AAA32997.1; -.
EMBL; J02798; AAA87348.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD002498; Napin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Seed storage protein; S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          its maturation.
                                                                                                                                                        SEQUENCE FROM N.A.
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es 5, Conserv
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              Brassica napus.";
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                                                                        REVISIONS
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PROPEP
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                                                                                                                                                                                              Crouch M.L., Tembarge K.M., Simon A.E., Ferl R.,
"CDNA clones for Brassica napus seed storage proteins: evidence from
nucleotide sequence analysis that both subunits of napin are cleaved
from a precursor polypeptide.",
J. Mol. Appl. Genet. 2:273-283(1983).
-!- FUNCTION: The small, basic, water-soluble napins are one of the
two major kinds of storage proteins synthesized in the seed during
                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: The mature protein consists of a small and a large chain linked by disulfide bonds.
-!- TISSUE SPECIFICITY: Cotyledons and the axis.
-!- SIMILARITY: Belongs to the 2S seed storage albumins family.
                Brassica napus (Rape).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica napus (Rape).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87308224; PubMed=3624251;
Josefsson L.-G., Lenman M., Ericson M.L., Rask L.;
"Structure of a gene encoding the 1.7 S storage protein, napin, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
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Pred. No. 5.3;
2; Mismatches 2; Indels
Napin 1 precursor (1.78 seed storage protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LARGE CHAIN.
SFDFC7ECE3E22ACB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (Rel. 10, Last sequence update)
01-AVG-1992 (Rel. 23, Last annotation update)
Napin 2 precursor (1.78 seed storage protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMALL CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003612; AAI.
InterPro; IPR000617; Napin.
Pfam; PF00234; tryp alpha_amyl; 1.
PRINTS; PR00496; NAPIN.
Probom; PD003498; Napin, 1.
SMART; SM00499; AAI; 1.
                                                                                                                                                            STRAIN=cv. Tower;
MEDLINE=84113267; PubMed=6689334;
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15294 MW;
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01-MAR-1989 (Rel. 10, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; K01544; AAA33005.1; -.
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                                                                                                                                                                                                                                                                                                                                                its maturation.
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A01330; NWRP1
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SEQUENCE Query Match

Matches

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RESULT 5 2SS2\_BRANA ID 2SS2\_BI

NON TER PROPEP

CHAIN CHAIN .

Gaps

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Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
-i- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.
-i- SUBCELLULAR LOCATION: Type II membrane protein.
-i- TISSUB SPECIFICITY: Natural killer cells.
-i- SIMILARITY: Contains 1 C-type lectin family domain.
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
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InterPro; IPR001304; Lectin_C.
Pfam; PF00059; Lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoutation update)
Tyrosinase precursor (EC 1.14.18.1) (Monophenol monooxygenase).
                                                                                                                                                                                                                                                               MEDLINE=20322487; PubMed=10866118; LaBonte M.L., Levy D.B., Letvin N.L.; LaBonte M.L., Levy D.B., Letvin N.L.; "Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A,
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
MKG2-D type II integral membrane protein (NKG2-D activating NK receptor) (NK cell receptor D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A44883F31400DEAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.0%; Score 35; 55.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                            Immunogenetics 51:496-499(2000).
                                                                                                                           Macaca mulatta (Rhesus macaque)
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25075 MW;
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DOMAIN 1 51
TRANSMEM 52 72
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Best Local Similarity 55...
For Si Conservative
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                                                                                                                                                                                        Cercopithecinae; Macaca.
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203
115
131
163
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202
216 AA;
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI TaxID=9544;
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P00440;
                                                                                                                                                                                                                                                                                                                                                             and D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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TYRO_NEUCR
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      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boutilier K.A., Gines M.J., Demoor J.M., Huang B.,
Baszczynski C.L., Iyer V.N., Miki B.L.,
"Expression of the BunNAP subfamily of napin genes coincides with the induction of Brassica microspore embryogenesis.",
Plant Mol. Biol. 26:1711-1723(1994)
-! FUNCTION! The small, basic, water-soluble napins are one of the two major kinds of storage proteins synthesized in the seed during its maturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBBUTE: The mature protein consists of a small and a large chain linked by disulfide bonds.
-!- TISSUE SPECIFICITY: Cotyledons and the axis.
-!- SIMILARITY: Belongs to the 2S seed storage albumins family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                           STRAIN=CV. Wester; IISSUE=Leaf;
MEDLINE-21346654; PubMed=2102844;
Bassczynski C.L., Fallis L.;
"Isolation and nucleotide sequence of a genomic clone encoding a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LARGE CHAIN.
6F3883CBED55FB26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 1;
Pred. No. 7.3;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seed storage protein; Signal; Multigene family.
          01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-EC-1998 (Rel. 37, Last annotation update)
Napin precursor (1.78 seed storage protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMALL CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003612; AAI.
InterPro; IPR00617; Napin.
Pfam; PF00234; tryp alpha_amyl; 1.
PRNUTS; PR06496; NAPIN.
ProDom; PD002498; Napin; 1.
SWART; SM00499; AAI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Topas;
MEDLINE=95161697; PubMed=7858212;
                                                                                                                                                                                                                                                                                                                                                  Brassica napus napin gene.";
Plant Mol. Biol. 14:633-635(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20318 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X17542; CAA35580.1; -. EMBL; U04945; AAA81909.1; -. PIR; S10018; S10018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.0%;
55.6%;
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CNIPQVSVC 169
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                                                                                                                       Brassica napus (Rape)
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180 AA;
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nes 5, Conserv
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                     NCBI_TaxID=3708;
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ID NKGD MACMU
AC Q9MZJ7;
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<u>8</u>

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Gaps

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Indels

161

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RESULT 7

SEQUENCE Query Match

Best Loc Matches

PROPEP ROPEP

SIGNAL CHAIN 0

Sun

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                                                                                                                                                                                                                                                                                                                     STRAIN-TS, and Sing;
MEDLINE=82190019; PubMed=6210697;
Ruegg C., Ammer D., Lerch K.;
Comparison of amino acid sequence and thermostability of tyrosinase from three wild type strains of Neurospora crassa.";
J. Biol. Chem. 257:6420-6426(1982).
-!- FUNCTION: THIS IS A COPPER-CONTAINING OXIDASE THAT FUNCTIONS IN THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
                                                                                                                                                                                                                                         "Primary structure of tyrosinase from Neurospora crassa. II. Complete amino acid sequence and chemical structure of a tripeptide containing an unusual thioether.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COULD BE INVOLVED IN ENZYME ACTIVATION. ACETYLATION.
              Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: L-tyrosine + L-DOPA + O(2) = L-DOPA +
                                                                                STRAIN=TS, and Oak Ridge;
MEDLINE=90008884; PubMed=2529259;
Kupper U., Niedermann D.M., Travaglini G., Lerch K.;
"Isolation and characterization of the tyrosinase gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008922; Di-Copper centre.
InterPro; IPR00223; Tyrosinase.
PERM: PR00264; tyrosinase; 1.
PRINTS; PR00092; TYROSINASE.
PROSTITE; PS00499; TYROSINASE 1; 1.
Melanin biosynthesis; Oxidoreductase; Monooxygenase; Copper; Acetylation; Thioether bond.
INIT MET 0 0 TYROSINASE.
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPPER A (BY SIMILARITY).
COPPER A (BY SIMILARITY).
COPPER B (BY SIMILARITY).
2'-(S-cysteinit).
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D -> E (IN STRAIN OR).
E -> T (IN STRAIN SING).
KS -> NN (IN STRAIN SING).
I -> T (IN STRAIN SING).
K -> N (IN STRAIN OR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOPAGUINONE + H(2)O.
COFACTOR: Binds 2 copper ions per subunit (By si
MISCELLANEOUS: THE STRAIN TS SEQUENCE IS SHOWN.
SIMILARITY: Belongs to the tyrosinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYROSINASE.
                                                                                                                                                       Biol. Chem. 264:17250-17258(1989).
                                                                                                                                                                                                                                                                                Biol. Chem. 257:6414-6419(1982)
                                                                                                                                                                                               STRAIN=TL;
MEDLINE=82190018; PubMed=6210696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M32843; AAA33619.1; -.
EMBL; M33271; AAA33618.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407
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1105
2777
281
306
14
130
130
346
423
                                                                                                                                         Neurospora crassa.";
  Neurospora crassa.
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                SEQUENCE OF 1-407.
                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-407
                                          NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOUNDS.
                                                                                                                                                                                                                        Lerch K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
CROSSLNK
VARIANT
VARIANT
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MOD_RES
METĀL
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METAL
METAL
METAL
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similarity).

(Cys-His).

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STRAIN-CSTBL/60: TISSUB-Embryo;

X MEDLINE-21085660; PubMed-11217851;

X MAN J. Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., X Mawi J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., X Arawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., A Satro T., Okazaki Y., Goloori T., Bono H., Kasukawa T., Saito R., A Satro T., Okazaki Y., Goloori T., Bono H., Kasukawa T., Saito R., A Satro T., Okazaki Y., Goloori T., Bono H., Kasukawa T., Saito R., A Sadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., A Sakai H., Sato K., Schoebbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Sato K., Schoebbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Maxarakhiari, V., Wanshiwa B., Marsakhiari, V., Voshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA SEQUENCE FROM N.A.

RA MEDLINE=22388257; PubMed=12477932;

RA Altaspherg R.L., Felingold B.A., Grouse L.H., Derge J.G.,

RA Altaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altachal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Frowrstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length

RY Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                       SYR MOUSE STANDARD, PRT; 660 AA.
09D019; QBVDM1;
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                               ..
                                                                                        70.0%; Score 35; DB 1; Length 620; 75.0%; Pred. No. 27; 1.1ve 2; Mismatches 0; Indels
449 449 K -> R (IN STRAIN OR).
234 234 N -> D (IN REF. 2 AND 3).
620 AA; 68546 MW; D12A30BB6A01D312 CRC64;
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
                                                                                                                                                                                                                              589 TVPLTSLC 596
                                                                                                                                                                                 2 SVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                        9
VARIANT
CONFLICT
SEQUENCE
                                                                                        Query Match
                                                                                                                                 Matches
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Pfam; PF00234; tryp alpha_amyl; 1.
PRINTS; PR00496; NAPIN.
ProDom; PD002498; Napin; 1.
LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 44.7.
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 CNIPRVSIC 119
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SMART; SM00499; AAI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica napus (Rape)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSVPLTSVC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRANA
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VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                             NON CONS
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          SPT TT WE WE SET TO SET
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                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALLI BRAJU STANDARD; PRT; 129 AA.
P80207; P80215;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-2003 (Rel. 42, Last sequence update)
Allergen Bra j 1-E, small and large chains (Bra j I).
Brassica juncea (Leaf mustard) (Indian mustard).
Brassica juncea (Leaf mustard) (Indian mustard).
Brassica juncea (Leaf mustard) (Indian mustard).
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                            diphosphate + L-arginyl-tRNA(Arg).
-!- SUBUNIT: Monomer; also part of a multisubunit complex that groups
tRNA ligases for Arg, Asp, Glu, Gln, Ile, Leu, Lys, Met and Pro.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- DOMAIN: The N-terminal (AA 1-72) has two regions predicted to be
alpha-helical that might be involved in the multisynthetase
                                                                                                                                                                                                         -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
               CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1914297; Rars.
Interpro; IPR001278; Arg_tRNA-synt_lc.
Interpro; IPR005148; N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AK011383; BAB27583.1; -. EMBL; BC020132; AAH20132.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 CSVPLTIV 376
                                                                                                                                                                                            complex assembly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence motif.";
Eur. J. Blochem. 197:741-746(1991).
-!- FUNCTION: The small, basic, water-soluble napins are one of the
two major kinds of storage proteins synthesized in the seed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: The mature protein consists of a small and a large chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ericson M.L., Muren E., Gustavsson H.O., Josefsson L.G., Rask L.; "Analysis of the promoter region of napin genes from Brassica napus demonstrates binding of nuclear protein in vitro to a conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linked by disulfide bonds.
-!- TISSUE SPECIFICITY: Cotyledons and the axis.
-!- SIMILARITY: Belongs to the 2S seed storage albumins family.
             -!- SIMILARITY: Belongs to the 2S seed storage albumins family. PIR; S35591, S35591.

InterPro; IPR003612; AAI.

InterPro; IPR003617; Napin. PRINTS; PR00496; Napin. PRINTS; PR00496; Napin. PRODOW; PR002498; Napin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.0%; Score 34; DB 1; Length 129; 44.4%; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                             6 6 F -> I.
20 20 R -> K.
129 AA; 14644 MW; D6F28E03F62E08F8 CRC64;
-!- ALLERGEN: Causes an allergic reaction in human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Napin B precursor (1.7S seed storage protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                        LARGE CHAIN.
F -> I.
R -> K.
                                                                                                                                                                                                                                                                                              SMALL CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-cv. Svalofs Karat 20516-K;
MEDLINE-91231016; PubMed=2029903;
                                                                                                                                                                                                               Problom; ruccerrate SMRRT; SM00499; AAI; 1.
Allergen; Seed storage protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X58142; CAA41150.1; -. PIR; S15382; S15382. Interpro; IPR003612; AAI. Interpro; IPR00617; Napin.
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                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Microbiol. 16:977-989(1995).
-!- FUNCTION: PROBABLY INVOLVED IN POLYMERIZATION AND/OR EXPORT OF EXOPOLYSACCHARIDE EPS I WHICH FUNCTIONS AS A VIRULENCE FACTOR.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02563; Poly export; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG.
Polysaccharide transport; Transport; Outer membrane; Transmembrane; Lipoprotein; Porin; Signal; Palmitate.
SIGNAL 1 23 POTENTIAL.
                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
EPS I polysaccharide export outer membrane protein epsA precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molécular characterization of the eps gene cluster of Pseudomonas solanacearum and its transcriptional regulation at a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarityj.
N-palmitoyl cysteine (By similarity).
BE0084252E819309 CRC64;
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0
                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPS I POLYSACCHARIDE EXPORT OUTER MEMBRANE PROTEIN EPSA.
                                                                                                                       Score 34; DB 1; Length 178;
Pred. No. 11;
                    BY SIMILARITY.
BY SIMILARITY.
SMALL CHAIN (BY SIMILARITY).
                                                                          LARGE CHAIN (BY SIMILARITY). 96CE0ADB7CD966E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-diacylglycerol cysteine (By
                                                                                                                                                       Indels
    Signal; Multigene family; Embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE BEXD/CTRA/VEXA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                        Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                        377 AA
                                                              BY SIMILARITY.
                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
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InterPro; IPR000437; Prok_lipoprot_S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96059643; PubMed=7476194;
                  21 BY
38 BY
74 SM
94 BY
178 LA
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                                                                                                                       68.0%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderiaceae; Ralstonia.
                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                           159 ČKIPQVSVČ 167
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 Seed storage protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S77634; S77634.
                                                                                        178 AA;
                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                              1 CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter."
                                                                                          SEQUENCE
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                                                            PROPEP
                               PROPEP
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                                                                          CHAIN
                                              CHAIN
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EPA2 RALSO
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MEDLINE-22486644. PubMed-12488443;
Miggin S.M., Lawler O.A., Kinsella B.T.;
Miggin S.M., Lawler O.A., Kinsella B.T.;
"Palmitoylation of the human prostacyclin receptor. Functional
implications of palmitoylation and isoprenylation.";
J. Biol. Chem. 278:6947-6558 (2003)
--- FUNCTION: Receptor for prostacyclin (prostaglandin I2 or PGI2).
The activity of this receptor is mediated by G(s) proteins which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakagawa O., Tanaka I., Usui T., Harada M., Sasaki Y., Itoh H., Yoshimasa T., Namba T., Narumiya S., Nakao K.; "Molecular cloning of human prostacyclin receptor cDNA and its gene expression in the cardiovascular system."; Circulation 90:1643-1647(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=95394450; PubMed=7665161;
Ogawa Y., Tanaka I., Inoue M., Yoshitake Y., Isse N., Nakagawa O., Usui T., Itoh H., Yoshimasa T., Narumiya S.;
"Structural organization and chromosomal assignment of the human prostacyclin receptor gene.";
Genomics 27:142-148(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activate adenylate cyclase.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Warren C.M., Aronstam R.S., Sharma S.V.; "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94216134; PubMed=7512962;
Boie Y., Rushmore T.H., Darmon-Goodwin A., Grygorczyk R.,
Slipetz D.M., Metters K.M., Abramovitz M.;
"Cloning and expression of a cDNA for the human prostanoid IP
                                                                                                                                                                 vi-NVV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prostacyclin receptor (Prostanoid IP receptor) (PGI receptor)
(Prostaglandin I2 receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Narumiya S., Ichikawa A.; "Cloning and expression of a cDNA for the human prostacyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=94237286; PubMed=7514139;
Katsuyama M., Sugimoto Y., Namba T., Irie A., Negishi M.,
Narumiya S., Ichikawa A.;
                                                                                                                         386 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 269:12173-12178(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Lung;
MEDLINE=95008086; PubMed=7923647;
                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 344:74-78(1994).
                                                                                                                         STANDARD;
                         16 CAVPLMAAC 24
                                                                                                                                                   01-NOV-1995 (Rel. 32,
01-NOV-1995 (Rel. 32,
                                                                                                                                                                                                                                                            Homo sapiens (Human)
1 CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE=Placenta;
                                                                                                                                                                                                                                             PTGIR OR PRIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALMITOYLATION
                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung;
                                                                                                                       HUMAN
                                                                                                                                        P431\overline{1}9
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Gaps

0

Score 34; DB 1; Length 377; Pred. No. 25; 2; Mismatches 2; Indels

68.0%; 55.6%;

Query Match

Local Similarity 55.6 les 5, Conservative

Best Loca Matches

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Ratausper R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,
RA Distrenko L., Marvaina K., Farmer A.A., Rubin G.M., Hong L.,
RA Distrenko L., Marvaina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Milalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glübs R.A.,
RA Millalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glübs R.A.,
RA Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schwutz S.M., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RY "Generation and initial analysis of more than 15,000 full-length
RT "Generation and initial analysis of more than 15,000 full-length
RT "Generation and initial analysis of sucre than 15,000 full-length
RT "Generation and initial analysis of sucre than 15,000 full-length
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RT "Generation and initial analysis of sucre than 15,000 full-length
RT "Generation and initial analysis of sucre than 15,000 full-length
Stress-activated proctein kinase (IKK)-dependent mechanism and
stress-activated proctei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Colon;
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                "Cloning and characterization of two overlapping genes in a subregion at 621 involved in replicative senescence and schizophrenia."; Gene 252:217-225(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Leonardi A., Chariot A., Claudio E., Cunningham K., Siebenlist U.; "CIKS, a connection to Ikappa B kinase and stress-activated protein
                                                                                                                                                                                                               TISSUE=Embryonic kidney;
MEDLINE=20442402; PubMed=10962024;
Li X., Commane M., Nie H., Hua X., Chatterjee-Kishore M., Wald D.,
Li A., Sark G.R.;
"Actl, an NF-Kappa B-activating protein.";
Proc. Natl. Acad. Sci. U.S.A. 97:10489-10493 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=1242403; PubMed=10962033; MEDLINE=20442403; PubMed=10962033; Theorem E., Siebenlist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                 MEDLINE-20363742; PubMed-10903453;
Morelli C., Magnanini C., Mungall A.J., Negrini M.,
Barbanti-Brodano G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 97:10494-10499 (2000)
  [1] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2).
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                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Uterus;
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                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kinase.
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                                                                                                                                                                                                                                                                                                                                                                      MIM; 600022; -. C.integral to plasma membrane; TAS. 60, 90:0005887; F.prostaglandin I receptor activity; TAS. 60; 90:0007267; F.prostaglandin I receptor activity; TAS. 60; 90:0007267; P:cell-cell signaling; TAS. 60; 90:0007187; P:G-procein signaling; coupled to cyclic nucl. . .; TAS. InterPro; IPR000376; GPCR Rhodgen. InterPro; IPR008365; ProstanoidR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIKS HUMAN STANDARD; PRT; 574 AA.
043734; Q9H5W2; Q9H6Y3; Q9NS14; Q9UG72;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adapter protein CIKS (Connection to IKK and SAPK/JNK) (Nuclear factor NP-Kappa-B activator 1) (ACT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERUTS; PR00201; 7tm 1; 1.

PRINTS; PR00217; GFCRRHODOPSN.

PRINTS; PR01788; PR0STANOIDR.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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7 (POTENTIAL).
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S-palmitoyl cysteine.
N-LINKED (GLCNAC. .)
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CYTOPLASMIC (1
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                                                                                                                                                                                                          EMBL, D25418; BAA05008.1; -.
EMBL, D29634; BAA06110.1; -.
EMBL, D38127; BAA07325.1; -.
EMBL, D38128; BAA07325.1; -.
EMBL, A574134; AA092301.1; -.
PIR, A57066; A57066.
Genew; HGNC:9602; PTGIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40955 MW;
                                                                                                                                                                                            EMBL; L29016; AAA36448.1; -.
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Matches 6; Conservative
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251 CSLPLTIRC 259
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LIPID CARBOHYD SEQUENCE

Query Match

CIKS HUMAN RESULT 14

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inhibitor.";
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                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last amortation update)
CDK5 regulatory subunit associated protein 1 (CDK5 activator-binding
Protein C42).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21975289; PubMed=11882646;
Ching Y.-P., Pang A.S.H., Lam W.-H., Qi R.Z., Wang J.H.;
"Identification of a neuronal Cdk5 activator-binding protein as Cdk5
                                                                                                                                                                                                                                                                                                                                                                                        HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20184747; PubMed=10721722;
Ching Y.-P., Qi Z., Wang J.H.;
"Cloning of three novel neuronal Cdks activator binding proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                              /FIId=VSP_004163.
Q -> H (IN REF. 1; AAF67445, 2 AND 4).
E -> D (IN REF. 3; AAF67447).
P -> S (IN REF. 1; AAF67447).
MISSING (IN REF. 6; BAB15117).
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                                                                                                                                                                                                                                                                                                                                                  MIM; 607043; -
GO; GO:0007242; P:intracellular signaling cascade; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64657 MW; E9857DEA5E349094 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND INTERACTION WITH CDKSR1 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             586 AA.
           Name=2; Synonyms=C6ORF5,
IsoId=O43734-2; Sequence=VSP_004163;
TISSUE SPECIFICITY: Widely expressed.
 IsoId=043734-1; Sequence=Displayed;
                                                                                                                                                                                                      AF274303; AAG15367.1; -.
AF272151; AAG15407.1; -.
AL008730; CAAL5506.1; -.
AL008730; CAAL5507.1; -.
AL008730; CAA15507.1; ALT_INIT.
                                                                                                                                                                                                                                                                              AK025351; BAB15117.1; -... AK026602; BAB15507.1; ALT_INIT. BC002823; AAH02823.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                     Missing
                                                                                                                                                                    EMBL; AF136405; AAF67445.1; -.
EMBL; AF136406; AAF67446.1; -.
EMBL; AF136407; AAF6747.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85./3,
--hog 6; Conservative
                                                                                                                                                                                                                                                                                                                  PIR; T08794; T08794.
Genew; HGNC:1343; C6orf4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
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225 LPLTSVC 231
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574 AA;
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CONFLICT
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EMBL;
EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                        EMBL;
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CSP1_RAT
ID AC Q9JUH
DT 10-OCT
DT 10-OCT
DT 10-OCT
DE CDKS:
CS RATTU
OC MAMMA:
OC MAMMA:
OC MAMMA:
COX NCB1.
RP SEQUE
RR TISSU
RX MEDLI:
RA Gene
RR Gene
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
1. Biol. Chem. 277:15237-15240(2002).

2. - FUNCTION: Probable regulator of CDKS activity. May inhibit CDKS clucked view at the interaction with CDKSR1.

2. - SUBDNIT: Interacts with CDKSR1 and CDKSR2. The interaction with CDKSR1 is prevented by the association between CDKSR1 and CDKSRAP2. Interacts also with the complex CDKSR1. Does not interact with monomeric CDKS. The interaction is prevented by the association between CDKSR1 and CDKSRAP2.

2. CDKSRAP2. Interacts also with the complex CDKSR1-CDKS. Does not interact with monomeric CDKS. The interaction is prevented by the association between CDKSR1 and CDKSRAP2.

3. CC -1-DOMAIN: The C-terminal part (475-586) is necessary for the interaction with CDKSR1, while the N-terminal part (1-168) is required for inhibiting the activity of the CDKS kinase.

3. SIMILARITY: CONTAINS 1 TRAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00729; Elp3; 1.
TIGRFAMs; TIGR01574; miaB-methiolase; 1.
TIGRFAMs; TIGR00089; TIGR00089; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65866 MW;
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Job time : 6.09091 secs
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OM protein -

Run on:

Sequence:

Searched:

Database

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                                                                                                                  5, 2004, 09:46:09; Search time 20.3636 Seconds (without alignments) 139.448 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                      1017041
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                            1017041 seqs, 315518202 residues
                                                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPTREMBL_25:*
1: Sp archea:*
2: sp_bacteria:*
3: sp fung1:*
4: sp human:*
5: sp invertebrate:*
5: sp mammal:*
5: sp mammal:*
5: sp mammal:*
5: sp organelle:*
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                     BLOSUM62
                                                                                                                                                                                                             Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

unclassified: \*

sp\_bacteriap:\*

rvirus:\*

sp archeap:\*

sp\_virus:\* sp\_vertebrate:\*

sp\_plant:\*
sp\_rodent:\*

	Description	06200 min min 06200						OBYKY PARKONS SP.					Colon arabidopsis	Organ arabidopsis	Coast # mernanococc	Qewrws homo sapien	Q9h6r1 homo sapien	Q9h747 homo sapien
SUMMARIES	ΩI	062028	OSZLE3	082258	083780	O8FCN4	063791	OBRXR2	O9ARC9	O9ARC6	O9ARF2	SARM3	091.00	058874	C Butting	Convers	Сунькі	Q9H747
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Q9h747 homo sapien

OBtb22 homo sanien	OBCIMO Versinia ne		094if5 orvza sativ	Ogv6a0 drosophila	O9d179 mus misculii	O96ba7 homo sanien	homo		chla	Ogulls homo ganien	001768 caenorhabdi	0	brassica	braggina	brassica			sinania ainania	Sinanis		sinapis	raphanis	sarcophaga	4	hrassica			brassica
4 Q8TB22	16 08CLM0	6 Q8HZR8	10 Q94JF5	5 Q9V6A0	11 Q9D179	4 Q96PA7		4 Q9BXN2	0	4 Q9ULL5	5 001768	10 Q9S9F0	10 Q9S9E7	10 Q9S9E9	10 Q9S9E8	16 Q97HY9	10 P80208	10 041278		10 041280		10 Q41167	5 Q9NL63	10 Q39344		10 042491		10 Q42413
802	97	247	718	1977	124	168		247	591	1217	2192	98	88	88	88	91	125	145			145	155	168	178	œ	178	178	178
76.0	74.0	74.0	74.0	74.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0
38	37	37	37	37		36	36	36	36	36	36	35	35	35	35	35	35	35	35	35	32					32	35	35
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. The Structural comparison of phospholipase-A2-binding regions in MEDLINE-95010128 bubMed=7925459;

A Higashino K., Ishizaki J., Kishino J., Ohara O., Arita H.;

A Higashino K., Ishizaki J., Kishino J., Ohara O., Arita H.;

A Higashino K., Ishizaki J., Kishino J., Ohara O., Arita H.;

B The Structural comparison of phospholipase-A2-binding regions in Structural comparison of phospholipase-A2-binding regions in Brit. J. Biochem. 225.375-382 (1994).

B B Lik. 348719; SHA06443.1; -.

B RBL; D30779; BAA06443.1; -.

B RSP; P02751; PRO0642; F: receptor activity; IEA.

B ROO6529; F: sugar binding; IEA.

B RINTERPO: IPRO09997; RicinB like.

B RINTS; PRO0013; FNTYPEII.

B RAMATI; SMO00495; FNZ; II; 1.

B RAMATI; SMO0199; FNZ; II; 1.

B RAMATI; SMO0199; FNZ; II; 1.

B RAMATI; SMO0199; RICIN; 1. 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) PRT; 1487 AA. Phospholipase A2 receptor precursor. PRELIMINARY; NCBI\_TaxID=10090; Q62028 Q62028; **262028** 

Wain J.,

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083380
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ö
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                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
STRAIN=LT2 / SGSC1412 / ATCC 700720;
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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Enterobacteriaceae; Salmonella.
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                                                                      DB 11; Length 1487;
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                             SIGNÄL 1 26 POTENTIAL.
CHAIN 27 1487 PHOSPHOLIPASE AZ RECEPTOR.
SEQUENCE 1487 AA; 170511 MW; ADBD905859B0EDE8 CRC64;
                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE008865; AAL22442.1; -.
InterPro; IPR002549; UPP0118.
Pfam; PP01594; UPP0118.
Hypothetical protein; Complete proteome.
SEQUENCE 349 AA; 38301 MW; 21A55D9F2C5FDB9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                        (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 AA.
                                                                                                                                                                                      349 AA
                                                                       Score 43; DB 1
Pred. No. 6.5;
1; Mismatches
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  PS50231; FICIN_B_LECTIN; 1.
                                                                                                                                                                                      PRT;
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MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;
                                                                                                                                                                                               QBZLE3;
01-MAR-2002 (TrEMBLrel. 20, Cr
01-MAR-2002 (TrEMBLrel. 20, La
01-JUN-2002 (TrEMBLrel. 21, La
Putative PerM family permease.
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                                                                       86.0%;
77.8%;
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                             7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001)
                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                              Salmonella typhimurium
                                                                                                                                    929 CSVPLPSIC 937
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                                                                                                                1 CSVPLTSVC 9
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                                                                         Query Match
Best Local Similarity
                   Receptor; Signal.
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Salmonella typhi
                                                                                                                                                                                                                                                  YHHT OR STM3582
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  PROSITE;
PROSITE;
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                                                                                             Matches
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Q8Z258
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Q8ZLE3
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SEQUENCE FROM N.A.

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STRAIN=Ty2 / ATCC 700931;

MEDINRE-25231367; PubMed=12644504;

MEDINRE-25231367; PubMed=12644504;

A Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

T "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2

T and CTLS.";

D Bacteriol. 185:2330-2337(2003).

R EMBL; ALGS-7281; CADD804811; -..

R EMBL; ALGS-7281; CADD804811; -..

R PRBL; AE016847; AAO71411.1; -..

R PRBL; AE01554; UPF0118; 1.

R PRBL; ARO1554; UPF0118.

R PRBL; ARO1554; UPF0118.

R PRBL; ARO1554; UPF0118.

R PRBL; ARO16118; Complete proteome.

W Hypochetical protein; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=301 / Serotype 2a, MEDLINE=22272406; PubMed=12384590; Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang Y., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Minchead S., Barrell B.G.; enterica serovar Typhi CI18.";
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STRAIN=2457T / ATCC 700930 / Serctype 2a;
STRAIN=2457T / ATCC 700930 / Serctype 2a;
STRAIN=245074; PubMed=12704152;
Weblink=22590274; PubMed=12704152;
Weblink=2590274; PubMed V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
Schwartz D.C., Blattner F.R.,
"Complete genome sequence and comparative genomics of Shigella
"Complete genome sequence and comparative genomics of Shigella
Ileareri serctype 2a strain 2457T.";
Infect. Immun. 71:2772-2786(2003).
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Enterobacteriaceae; Shigella.
NCBI_TaxID=623;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annocation update)
01-OCT-2003 (TrEMBLrel. 25, Last annocation update)
0rf, conserved hypothetical protein (Hypothetical protein yhhT)
YHHT OR SF3492 OR S4271.
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Best Local Similarity luv...
8; Conservative
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SEQUENCE FROM N.A.

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

A Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,

A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin B., Lin B., Lin B., Lin B., Lin B., Lin B., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

Theologis A.,

Theologis A.,

Thabidopsis Full Length cDNA Clones.";

K Submitted (FBB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AV080722; AAL86324.1;

DR GO; GO:0016020; C:membrane; IEA.

GO; GO:0016021; F:voltage-gated chloride channel activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                             82.0%; Score 41; DB 11; Length 409; 66.7%; Pred. No. 5.1;
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                                                                                                                                                                                                                                        409 AA; 47740 MW; 56D957D2DCA00AD8 CRC64;
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SMART; SM00116; CBS; 2.
Hypothetical protein.
SEQUENCE 585 AA; 62547 MW; E29CE5844B81D826 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                   GO, GO:0004872; F:receptor activity; IEA.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IRROll34; Lectin_C.
Pfam; PF00059; lectin_c; 3.
SMART; SM00034; CLECT; 3.
PROSITE; PS50041; C_TYPE_LECTIN_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000644; CBS domain.
InterPro; IPR001807; Cl-Channel volt.
Pfam; PF00571; CBS; 2.
Pfam; PF00654; voltage CLC; 1.
                     Eur. J. Biochem. 225:375-382(1994).
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                                    EMBL; D30781; BAA06445.1; -. HSSP; P23807; 1IXX.
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Best Local Similarity 100...
Best Similarity 100...
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Best Local Similarity
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NON TER
SEQUENCE
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XM MEDLINE=22388234; PubMed=12471157;

A Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

A Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

A Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

A Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

T "Extensive mosaic structure revealed by the complete genome sequence RL proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

REMEL, AEO16768; AANN2773.1; -

DR FMEL, RED16768; AANN2773.1; -

DR Ffam, PF01594; UPF0118; 1.

KW Hypothetical protein; Complete protecome.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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MEDLINE=95010128; PubMed=7925459;
Higashino K., Ishizaki J., Kishino J., Ohara O., Arita H.;
"Structural comparison of phospholipase-A2-binding regions in phospholipase-A2 receptors from various mammals.";
                                                                                                                 82.0%; Score 41; DB 16; Length 349;
100.0%; Pred. No. 4.4;
iive 0; Mismatches 0; Indels
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EMBL; AE016992; AAP19231.1; -.
InterPro; IPR002549; UPP0118.
Pfam; PF01594; UPP0118; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 349 AA; 38464 MW; 935ADBAB5ED65651 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                         376 AA
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Best Local Similarity 100.v.
                                                                                                                                Best Local Similarity 100.
Matches 8; Conservative
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263.791
1D 63.77
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Hypothetical protein.
SEQUENCE 750 AA; 79985 MW; 928E6D1EE2E5FCD4 CRC64;
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SMART, SM00116; CBS; 2.
Hypothetical protein.
                                      82.0%;
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                                                              Conservative
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780 AA; 8
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Best Local Similarity '
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NCBI_TaxID=81985;
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                                                                                                                                                                                                                                                                                                                                                                                               genomes."
                                                                                                                                                                                       Q9ARF2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9ARM3
                                                                                                                                                                            Q9ARF2
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                                                                                                                                                   RESULT 10
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                 01-UTN-2001 (TYEMBLrel. 17, Created)
01-UTN-2001 (TYEMBLrel. 17, Last sequence update)
01-OTT-2003 (TYEMBLrel. 25, Last annotation update)
Hypothetical protein.
Lycopersicon esculentum (Tomato).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rossberg M., Theres K., Acarkan A., Herrero R., Schmitt T., Schumacher K., Schmitz G., Schmidt R., "Comparative sequence analysis reveals extensive microcolinearity in the Lateral supressor regions of the tomato, Arabidopsis and Capsella
                                                                                                                                           AEQUENCE FROM N.A.
MEDLINE-21178822; PubMed-11283350;
Rosabberg M., Theres K., Acarkan A., Herrero R., Schmitt T.,
Schumacher K., Schmitt S., Schmitt R.;
"Comparative sequence analysis reveals extensive microcolinearity in the lateral supressor regions of the tomato, Arabidopsis and Capsella
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomes.";
Plant Cell 13:979-988(2001).
Plant Cell 13:979-988(2001).
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.
GO; GO:0006821; P:chloride transport; IEA.
Interpro; IPR000644; CBS domain.
Interpro; IPR001807; Cl-channel_volt.
PF00571; CBS; 2.
                                                                                                                                                                                                                   genomes.";
plant (cell 13:979-988(2001).
EMBL, AJ303344; CAC36598.1; -.
GO, GO:0016020; C:membrane; IEA.
GO, GO:0005821; F:volteage-gated chloride channel activity; IEA.
GO, GO:0006821; P:voltoride transport; IEA.
InterPro; IPR000644; CBS domain.
InterPro; IPR001807; Cl-channel_volt.
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                                                                                                                                                                                                                                                                                                                                                                                                 82.0%; Score 41; DB 10; Length 750;
100.0%; Pred. No. 8.8;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEGUENCE 750 AA; 79994 MW; 400448EB3D37042C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          750 AA.
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01-JUN-2001 (TrEMBLrel. 17, Created)
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PRINTS; PR00762; CLCHANNEL.
SMART; SM00116; CBS; 2.
                                                                                                                                                                                                                                                                                                                  Pfam; PF00571; CBS; 2.
Pfam; PF00654; voltage CLC; 1.
PRINTS; PR00762; CLCHANNEL.
SWART; SM00116; CBS; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 CSVPLTSV 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSVPLTSV 8
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                      NCBI TaxID=4081;
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UTM-2001 (TrEMBLrel. 17, Created)
01-UTM-2001 (TrEMBLrel. 17, Last sequence update)
01-UTM-2001 (TrEMBLrel. 25, Last sequence update)
01-OTC-2003 (TrEMBLrel. 25, Last sequence update)
01-OTC-2003 (TrEMBLrel. 25, Last sequence)
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
14-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Capsella rubella.
Eukaryota, Viidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Capsella.
                                                                     Gaps
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Rossberg M., Theres K., Acarkan A., Herrero R., Schmitt T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.0%; Score 41; DB 10; Length 780; 100.0%; Pred. No. 9.2; 0; Mismatches 0; Indels
Score 41; DB 10; Length 750;
Pred. No. 8.8;
                                                                        Indels
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EMBL, AJ303349; CRC36391.1; -.

EMBL, AJ303349; CRC36391.1; -.

GO; GO:001620; C:membrane; IEA.

GO; GO:000521; F:voltage-gated chloride chan

GO; GO:0006821; P:voltage-gated chloride chan

InterPro; IPR001644; CBS domain.

InterPro; IPR001647; Cl-channel_volt.

Pfam; PF00571; CBS; 2.

Pfam; PF00654; voltage_CLC; 1.
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                                         100.0%; Pred. No. 8.8
cive 0; Mismatches
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel 07, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                  [5]
SEQUENCE FROM N.A.
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                                                                                                                                                                     20 SEQUENCE FROM N.A.

21 SECURACE FROM N.A.

22 TISSUE-Seedling aerial parts;

23 Vihauger-Douard M., Charon C., Lapous D., Allot M., Granier F.,

24 A Vihauger-Douard M., Charon C., Lapous D., Allot M., Granier F.,

25 Buchez D., Barbier-Brygoo H., Ephritikhine G.;

26 Marbidopsis chloride channel.";

27 Tabaldopsis chloride channel.";

28 BmBL; Ass66388, Aak53391.1;

29 BmBL; Ass66388, Aak53391.1;

20 BmBL; Ass66388, Aak53391.1;

20 BmBL; Ass66388, Aak53391.1;

21 BmBL; Ass66388, Parts1991.1;

22 BmBL; Ass66388, Parts1991.1;

23 BmBL; Ass66388, Aak53391.1;

24 BmBL; Ass66388, Aak53391.1;

26 GO:0005247; F:volleage-gated chloride channel activity; IEA.

26 GO:0006821; P:chloride transport; IEA.

27 BmBL; Ass60889, Aak53391.1;

28 BmBL; Ass60889, Aak53391.1;

29 BmBL; Ass60889, Aak53391.1;

20 BmBL; Ass60889, Aak53391.1;

20 BmBL; Ass60889, Aak53391.1;

21 BmBL; Ass60889, Aak53391.1;

22 BmBL; Ass60889, Aak53391.1;

23 BmBL; Ass60889, Aak53391.1;

24 BmBL; Ass60889, Aak53391.1;

25 BmBL; Ass60889, Aak53391.1;

26 BmBL; Ass60889, Aak53391.1;

27 BmBL; Ass60889, Aak53391.1;

28 BmBL; Ass60889, Aak53391.1;

29 BmBL; Ass60889, Aak53391.1;

20 BmBL; Ass60889, Aak53391.1;

21 BmBL; Ass60889, Aak53391.1;

22 BmBL; Ass60889, Aak53391.1;

23 BmBL; Ass60889, Aak53391.1;

24 BmBL; Ass60889, Aak53391.1;

25 BmBL; Ass60889, Aak53391.1;

26 BmBL; Ass60889, Aak53391.1;

27 BmBL; Ass60889, Aak53391.1;

28 BmBL; Ass60889, Aak53391.1;

29 BmBL; Ass60889, Aak53391.1;

20 BmBL; Ass60889, Aak5389, Aak5399, Aak5399, Aak5399, Aak5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                 "Comparative sequence analysis reveals extensive microcolinearity in the Lateral supressor regions of the tomato, Arabidopsis and Capsella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
Shinn P., Altafi H., Bei Q., Chin C., Chiou U., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Shinn P.P., Buehler E.E., Dunn P.P., Feng J.J., Kim C.C., Li Y.Y.,
Walker M.M., Altafi H.H., Araujo R.R., Conn L.L., Conway A.A.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
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100.0%; Pred. No. 9.2;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              781 AA; 83548 MW; BE9DEB3603D9E0D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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Schumacher K., Schmitz G., Schmidt R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00654; voltage CLC; 1.
                                                                                                                          Plant Cell 13:979-988(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00762; CLCHANNEL.
SMART; SM00116; CBS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
1es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     514 CSVPLTSV 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSVPLTSV 8
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ecker J.R.;
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Matches
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09LG04
DD 09LG00
DT 01-OC
DT 01-OC
DD 
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A SEQUENCE FROM N.A.

A CHEUK R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
A Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
A Conn L., Corway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Conn L., Corway A., Gonzalez A., Liu J., Liu S., Mukharsky N.,
RA Lee J., Lenz C., Li J., Liu J., Liu J., Liu S., Mukharsky N.,
RA Thaveri A., Toriuni M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
B. Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
B. Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
B. Submitted (JUN-2000) to the E
Gonzalez A.A., Hansen N.N.F., Huizar L.L., Kremenetskaia I.I.,
Lenz C.C., Li J.J., Liu S.S., Luros S.S., Rowley D.D., Schwartz J.J.,
Toriumi M.M., Vysotskaia V.V., Yu G.G., Davis R.R.W.,
Federspiel N.N.A., Theologis A.A., Ecker J.J.R.,
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-JAL-1 / DSW 2661 / ATCC 43067;
STRAIN-JAL-1 / DSW 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=868807;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Scriton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Werbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.E., Puhrmann J.L., Nguyen D., Utcerback T.R., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                    Ecker J.R.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
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Hypothetical protein MJ1479.
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100.0%; Pred. No. 9.2
tive 0; Mismatches
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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
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R GO; GO:0005622; C:intracellular; IEA.

R GO; GO:0005840; C:ribosome; IEA.

R GO; GO:0005840; C:ribosome; IEA.

R GO; GO:0003735; F:l-aminocyclopropane-1-carboxylate synthase . . .;

R GO; GO:0003735; F:structural constituent of ribosome; IEA.

R GO; GO:0008483; F:transaminase activity; IEA.

R GO; GO:0006412; P:biosynthesis; IEA.

R GO; GO:0006412; P:piosynthesis; IEA.

R GO; GO:0006412; P:piosynthesis; IEA.

R GO; GO:0006412; P:piosynthesis; IEA.

R R GO; GO:0006412; R:Dosomal J G.

R Pfam; PF00155; aminotran 1 J II.

R PROSITE; PS01048; R:DSOSOMAL S6. I.

R PROSITE; PS01048; R:DSOSOMAL S6; I.

R PROSITE; PS01048; ACCSYNTHASE.

R PROSITE; PS01048; ACCSYNTHASE.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotherical protein FL/21969.
Homo sapiens (Human).
Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae; Homo.
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Hymos spiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.
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Pred. No. 13;
0; Mismatches 2; Indels
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Strausberg R.;
Strausberg R.;
Submitted (2004-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017468; AAH17468.1; -..
InterPro; IPR008928; Glyco_trans_6hp.
Hypothetical protein.
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Best Local Similarity 77.8%;
Matches 7; Conservative C
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Best Local Similarity
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Q8WVW3;
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RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequenching project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL, AK02562; BAB15192.1;
DR InterPro; IFR008928; Glyco_trans_6hp.
KW Hypothetical protein.
SQ SEQUENCE 491 AA; 54720 MW; 4F73721A9D092C37 CRC64;
Query Match
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Atches 6; Conservative 1; Mismatches 2; Indels 0; Gaps
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps
Oy 1 CSVPLTSVC 9
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Search completed: September 5, 2004, 10:00:01
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5, 2004, 09:37:49; Search time 29.5455 Seconds
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86.068 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                            protein search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Listing first 45 summaries

Post-processing: Minimum Match 08 Maximum Match 1008

Geneseq\_29Jan04;\*

Database

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2003bs:\* geneseqp2003bs:\*

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оķс	Query	100.0	86.0	78.0	78.0		.78.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0		76.0	76.0	76.0	0.00		0.4.1	74.0		74.0	•	72.0	•
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AAU19674	AAM43498	ABB10143	AAU18408	ABP47894	ABP66730	ADC10856	ADC46210	AAW52837	AAY27449	AAV41764	ANTI-2000	900071154	AAB44320	AAU29077	ABB90372	ABU58453	ARITABOOL		ABU84316	ABR66190	ABR65580	,
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36	36	36	36	36	36	36	36	36	36	36	36	36	2 (	36	36	36	36	20	36	36	36	
56	27	28	29	30	31	32	33	34	35	36	37	ď	0 0	ر د د	40	41	42	4.3	n F	44	45	

### ALIGNMENTS

Human; VEGF, vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. /note= "This bond cyclises the peptide" Cendron A; Location/Qualifiers 1...9 Stacker S, AAU04529 standard; peptide; 9 AA. VEGF based monocyclic peptide 7. (LUDW-) LUDWIG INST CANCER RES. 18-JAN-2001; 2001WO-US001533. 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. (first entry) Hughes RA, WPI; 2001-442248/47. Key Disulfide-bond WO200152875-A1. 26-SEP-2001 26-JUL-2001. Synthetic. AAU04529; Achen MG, AAU04529 

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, conversionation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, cretenional vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, had, heat or cold trauma, substance-induced medvascularisation of the liver, excessive cremina, substance-induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability or ammmal (the mammal has a condition characterised by fluid cor brain. The peptides are used to in lungs, peritoneal cavity, pleura, or brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere consulature inflammation with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9 AA;
                         $$$$$$$$$$$$$$$$$$$$$$$$$$$$
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100.0%; Score 50; DB 4; Length 9; 100.0%; Pred. No. 1.4e+06; 0; Indels 0; Mismatches 9; Conservative 1 CSVPLTSVC 9 Query Match Best Local Similarity Matches 9; Conserv g à

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Gaps · 0

> Murine phospholipase A2 receptor protein SEQ ID NO:7. AAB23826 standard; protein; 1487 AA. (first entry) 15-JAN-2001 AAB23826; RESULT 2 AAB23826

Endocytic C lectin family, B-selectin; type C lectin; identification. US6117977-A. 12-SEP-2000. Mus sp. 

96US-0052524P. 96US-00637021. 97US-00840062. 24-APR-1997; 24-APR-1996; 24-APR-1996;

(GETH ) GENENTECH INC.

WPI; 1997-535838/49.

Lasky LA;

Νu Κ,

Human and mouse type C lectin(s) - useful as competitive inhibitor of lectin activity and as molecular markers for tissues that express them Example; Fig 3; 72pp; English.

The present invention describes an isolated type C lectin polypeptide (I) comprising amino acid residues 37-133, 37-174, 175-229, 234-360, 381-507, 520-645, 657-809, 824-951, 970-1108, 1110-1243, or 1259-1393 of the protein sequence given in A23822. The first 2 polypeptides are capable of binding to a carbohydrate residue, and the rest of the polypeptides

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused in P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the

are useful for producing antibodies capable of binding to these 2 polymeptides. Polymucleotide sequence encoding the polypeptides of the invention are useful in the identification and purification of their native ligands, and as molecular markers of the tissues in which they are expressed. They provide valuable sequence motifs, which can be inserted or substituted into other native members of the endocytic type C lectins, and provide hybridisation probes for searching cDNA and genomic libraries for the coding sequence of other type C lectins. Variants of type C lectins may be used therapeutically as competitive inhibitors of the biological activity of native type C lectins. The present sequence represents a murine phospholipase A2 receptor protein which is homologous to a type C lectin ö SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant. Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for Gaps .; 0 Length 1487; Bhatia A; 1; Indels Propionibacterium acnes immunogenic protein #24583. Persing DH, Mitcham JL, Wang SS, e J, Zhang Y, Jen S, Carter D; 86.0%; Score 43; DB 2; I 77.8%; Pred. No. 1.3e+02; Example 1; SEQ ID NO 24882; 1069pp; English. 1; Mismatches AAU63687 standard; protein; 73 AA 21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P. 20-APR-2001; 2001WO-US012865. (first entry) Query Match Best Local Similarity 77.8° Local 7, Conservative Propionibacterium acnes. treating acne vulgaris. 929 CSVPLPSIC 937 WPI; 2001-616774/71. N-PSDB; AAS59634. 1 CSVPLTSVC 9 (CORI-) CORIXA CORP. L'maisonneuve J, Sequence 1487 AA; WO200181581-A2. 01-NOV-2001. 27-FEB-2002 Skeiky YAW, AAU63687; AAU63687 8×33333333333333 g à

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presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosobent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes predicted ORF-encoded polypeptide #24882.
                                                                                                                                                                                                                                                                                                                                                                                                                          Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                         Score 39; DB 4; Length 73;
Pred. No. 32;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        immunostimulant; immune response; vaccine
                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                         78.0%;
66.7%;
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                                                                                                                                                                         Query Match
Best Local Similarity 66.79,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003033515-A1.
                                                                                                                                                               Sequence 73 AA;
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Barth B,
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Maisonneuve JL; Jones R, Carter D; Bhatia A, Benson DR, Wang S, Jen s, Low Vallieve-Douglass J;

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention, antibodies against polypeptides of the invention; antibodies specific for a polypeptide of the invention; antibodies specific for a p. acnes method for stimulating an immune response specific for a p. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, antibodies, fusion proteins, T cell populations, or New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. Example 1; SEQ ID NO 24882; 1481pp; English.

WPI; 2003-381789/36. N-PSDB; ACF64563

antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and amethod for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the colypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for protein. The polynucleotides can also be used as probes or primers for antimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present reading frame) contained within the P. acnes polynucleotides of the canding frame) contained within the P. acnes polynucleotides of the cinvention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly the mipo at ftp.wipo.int/pub/published\_pot\_sequences 8×300000000000000×8

Sequence 73 AA;

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Gaps

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Gaps
                     ;
    Length 73;
                    2; Indels
 Score 39; DB 6;
Pred. No. 32;
1; Mismatches
 78.0%;
66.7%;
                  Conservative
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Query Match
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AAU53277 standard; protein; 88 27-FEB-2002 (first entry) AAU53277;

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Propionibacterium acnes immunogenic protein #14173.

SAPHO syndrome, synovitis, acne, pustulosis, hypertosis, osteomyelitis, uveitis, endophthalmitis, bone, joint, central nervous system, ELISA, inflammatory lesion, acne vulgaris, enzyme linked immunosorbent assay, dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes.

WO200181581-A2. 

20-APR-2001; 2001WO-US012865. 01-NOV-2001.

21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P.

(CORI-) CORIXA CORP.

Bhatia A; Mitcham JL, Wang SS, , Jen S, Carter D; Persing DH, M L'maisonneuve J, YAW, Skeiky

2001-616774/71. N-PSDB; AAS59559 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.

Example 1; SEQ ID NO 14472; 1069pp; English.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

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pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies of specific for P. acnes proteins. These antibodies can be used to down-equilate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by charge linked immunosorbent assay (BLISA). Note: The sequence data for this patent did not form part of the primited specification, but was obtained in electronic format directly from WIPO at the vipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention, antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes predicted ORF-encoded polypeptide #14472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 4; Length 88; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 14472; 1481pp; English.
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Barth B, Vallieve-Douglass J;
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Zhang Y, Wang S, Jen S,
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ses 6; Conservative
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Carter D;

Maisonneuve JL; Jones R, Carte

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method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared to polypeptide and an isolated T cell population constraints T cell spendations, or to polymulectides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymuclectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the proteins, T cell populations or antigen-presenting cells that express the proteins, or for stimulating an immune response specific for a P. acnes polypeptides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the connection of an immune response against P. acnes, or for treating acnet and the kit is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present canding frame) contained within the P. acnes polymuclectides of the creating frame) contained within the P. acnes polymuclectides of the printed specification, but was obtained in electronic format directly the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_esquences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 6; Length 88;
Pred. No. 39;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes immunogenic protein #4790.
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L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 5089; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU43894 standard; protein; 101 AA.
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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66.7%;
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 88 AA;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (synovitis, acne, particularis), uvertis and endophthalitis.

The disorders include SAPHO syndrome (synovitis, acne, and the cane) by acness is also involved in infections of bone, joints and the central revous system, however it is particularly involved in the inflammatory presence or absence of P. acnes in a patient comprises contacting a comple with a binding agent that binds to the proteins of the invention of sample with a binding agent that binds to the proteins of the invention of and determining the amount of bound protein in the sample. The complete and be used as antigens in the production of antibodies and determining the amount of bound activity of P. acnes polypeptides and compregulate expression and activity of P. acnes polypeptides and confined and activity of P. acnes polypeptides and confined and activity of P. acnes polypeptides and confined agents for determining P. acnes proteins for example, by the patent did not form part of the printed specification, but was for contained in electronic format directly from WIPO at
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1 CSVPLTSVC 9 Sequence 101 AA;

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ABM40413 ID ABM

ABM40413;

Propionibacterium acnes predicted ORF-encoded polypeptide #5089. (first entry) 20-OCT-2003 

Propionibacterium acnes.

WO2003033515-A1.

(CORI-) CORIXA CORP.

N-PSDB; ACF64450.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to

76.0%; Score 38; DB 4; Length 101; 66.7%; Pred. No. 66; 1; Mismatches 1; Indels 16 CNLPLTLVC 24 à 셤

ABM40413 standard; protein; 101 AA.

Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostīmulant; immune response; vaccine

24-APR-2003.

11-OCT-2002; 2002WO-US032727

15-OCT-2001; 2001US-00978825

Maisonneuve JL; Jones R, Carter D; , Bhatia A, Benson DR, Mitcham JL, Skeiky YAW, Persing DH, Zhang Y, Wang S, Jen S, Lodes MJ, Wang S, Jen S, Loge Vallieve-Douglass J; Zhang Y, Barth B,

2003-381789/36.

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. Example 1; SEQ ID NO 5089; 1481pp; English.

development abnormality. embryonic 

Claim 1; Page 30; 34pp; Chinese.

c immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a polymucleotide of the invention; antibodies against polypeptides of the invention; a method for stimulating an immune response specific for a P. acnes colypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polymenteleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient. The P. acnes polypeptides, polymelocides, antibodies, fusion proteins. T cell populations or antigen-presenting cells that express the polyments, or for treating and proteins, or cell populations or antigen-presenting or treating acnes protein. The polymucleotides an immune response specific for a P. acnes for undlating an immune response specific for a P. acnes protein. The polymucleotides can also be used as probes or primers for stimulation of an immune response against P. acnes, or for treating acnes the polymer of an immune response against P. acnes, or for treating acnes and the kit is useful for performing a diagnostic assay. The present reading frame) contained within the P. acnes polymelectides of the canding frame) contained within the P. acnes polymelectides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly the manner of the printed specification, but was obtained in electronic format directly and the polyment and pol Gaps .. DB 6; Length 101; 66; 1; Indels 2; Mismatches 76.0%; Score 38; 66.7%; Pred. No. 6; Conservative CNLPLTLVC 24 Q Best Local Similarity 1 CSVPLTSVC Sequence 101 AA; Query Match Matches

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RESULT 9 AAU74551

셤 8

AAU74551 standard; protein; 121 AA.

AAU74551;

08-MAY-2002 (first entry)

Human protein phosphatase 13.31 polypeptide.

Human; protein phosphatase 13.31; enzyme; malignant tumour; cancer; embryonic developmental abnormality; autoimmune disease; antisenescence; gynaecological; cytostatic; immunosuppressant; gene therapy.

Homo sapiens.

WO200212457-A1.

14-FEB-2002.

02-JUL-2001; 2001WO-CN001118.

07-JUL-2000; 2000CN-00117017.

(BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

Xie Y; Mao Y,

2002-172153/22. WPI; 2002-172153/ N-PSDB; ABK14072.

Human protein phosphatase 13.31 and encoding polynucleotide, used in diagnosis and treatment of malignant tumors, autoimmune disease and

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12-JUN-2001
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                                                                                                                                                                                                                                                       AAB74693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yue H,
                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                    AAB74693
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                                                                                                                                                             g
  888688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polymucleotide (I) and polypeptide (II) captenaces. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consistent in gene therapy techniques to restore normal activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding pattners are useful in medical imaging of sites expressing (II). (II) and its binding pattners are useful for treating disorders or polypeptide and polymucleotide sequences have applications in colypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations corresponsible for genetic disorders or other trails to assess blodiversity amino acid sequences. Abgono10-Abg30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this
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The invention relates to an isolated polypeptide of human protein phosphatase 13.31 and its associated polynucleotide. The sequences are used in diagnosis and treatment of malignant tumour, embryonic developmental abnormality and autoimmune disease and for studying human antisenescence. This sequence represents human protein phosphatase 13.31
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                             Length 121;
                                                                                                                                       2; Indels
                                                                                                             Score 38; DB 5;
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 41834; 103pp; English.
                                                                                                                              Pred. No. 78;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #11466.
                                                                                                                                                                                                                                                                ABG11475 standard; protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                               76.0%;
66.7%;
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                                                                                                                                           6; Conservative
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N-PSDB; AAS75662.
                                                                                                                                                                      1 CSVPLTSVC 9
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                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                       Sequence 121 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                        RESULT 10
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AAF81714 to AAF81740 encode the human proteases and protease inhibitors (PPIMS) given in AAB74668 to AAB74694. The PPIMS can have activities such as: anti-human immunodeficiency vitus (HIV); antidiabetic; antithyroid; immunostimulant; immunomodulator; antiinflammatory; immunosuppressive; nephrotropic; antigout; thyromimetic; cytostatic; antibacterial; thyridiate; protezozacide; antiarteriosclerotic; antiatherosclerotic; virucide; antipaciatic; and hepatotropic. PPIM polynucleotide and protein sequences can be used in the diagnosis, treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; protease; protease inhibitor; protease and protease inhibitor; ppIM; identification; diagnosis; anti-human immunodeficiency virus; HIV; antidabetic; immunostimulant; immunomodulator; antiinflammatory; antithyroid; immunosupressive; nephrotropic; antiinflammatory cycostatic; antibacterial; fundicide; protozoacide; antiarteriosclerotic; antiatherosclerotic; antipsoriatic; virucide; hepstotropic; gene therapy; autoimmune disorder; inflammatory disorder; AIDS; DiGeorge's syndrome; severe combined immunodeficiency disease; SCID; Chediak-Higashl syndrome; Crohn's disease; Addison's disease; autoimmune thyroiditis; gout; Crohn's disease; Mashimoto's thyroiditis; Sjogren's syndrome; infection; Crohn sease; sandrome; cancer; Werner's syndrome; call proliferative disorder; arteriosclerosis; atherosclerosis;
                                                                                                                                                                                                                                                                 0;
patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lu DAM;
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                                                                                                                                                                                                           Length 225;
                                                                                                                                                                                                                                                                    2; Indels
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                                                                                                                                                                                                           Score 38; DB 4; I pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protease and protease inhibitor PPIM-26.
                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB74693 standard; protein; 742 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2000; 2000WO-US021878.
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99US-0160807P.
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                Query Match
Best Local Similarity 66.,
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            209 ČŠVPITDPČ 217
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                                                                                                                                                 Sequence 225 AA;
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21-OCT-1999;
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Claim 11; Page 492-494; 567pp; English.

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                                            Crohn's disease, diabetes mellitus, Good pasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, Sjogren's syndrome, Werner's syndrome, viral, bacterial, fungal, parasitic, protozoal, and helminthic syndrome, cell proliferative disorder such as arteriosclerosis, polymucleotide sequences can be used in somatic or germline gene therapy and in diagnosis of diseases. They can also be used in generating sequences and in mapping the naturally occurring genomic sequences and in molecular biology techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; proliferative disorder; cancer; tumour; clotal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer* s disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; professional disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; chromosome 17; binding partner identification.
of autoimmune/inflammatory disorders such as AIDS, DiGeorge's syndrome, severe combined immunodeficiency disease (SCID), Chediak-Higashi syndrome, Cushing's disease, Addison's disease, autoimmune thyroiditis, Crohn's disease, diabetes mellitus, Good pasture's syndrome, gout,
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzhelmer's and Parkinson's diseases and cancers.
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                                                                                                                                                                                                                                                         Length 742;
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Pred. No. 4.6e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Human_mature_secreted_protein
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                              AAE01782 standard; protein; 802 AA.
                                                                                                                                                                                                                                             76.0%; Scor
66.7%; Prec
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30-JUN-2000; 2000US-0215140P.
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                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.,,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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| CSVPITDPC 734
                                                                                                                                                                                                                                                                                                                 1 CSVPLTSVC 9
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                                                                                                                                                                                                                  Sequence 742 AA;
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AMERICAND STANDS SERVING AND SECRET SERVING TO SERVING THE PROCESS.

C. Protein genes and AABO170-AABO1849 represent the proteins they encode. Decision of the secreted protein fragments or variants.

C. C. AABO1850-AABO1860 represent human secreted protein fragments or variants.

C. C. AABO1850-AABO1860 proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.

C. C. AABO1850-ABO1860 proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.

C. C. AABO1850-ABO1860 proteins are useful for preventing, treating the presence of mutations in the wide presence of mutations in the mew genes. Specific uses are described for each of the 28 genes, developing products for the diagnosis or treatment of proliferative disorders, tumours, foetal and developmental abnormalities, haematopoietic disorders, foetal and developmental abnormalities, haematopoietic disorders, edulopmental abnormalities, continued disorders, atheriopherial asthma, skind disorders, genticophenia, asthma, skind disorders, proteins disorders, diabotes atherosclerosis, cardiovascular disorders, prograndissis), sepsis, diabotes, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs to regenerate tissues, to identify their cognate ligands or binding to preservative to modify storage properties. Antibodies specific for a protein of the invantion of the invantion also be used to an heaved as a food additive or repenent of the invantion and an also be used in allowiating commenced as a food additive or repenent of the invantion of the invantion and an also be used to an also be used as a food additive or repenent of the invantion and an also be used as a food additive or repenent of the invantion and an also become a serviciated and an also become and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence represents a human secreted protein of the invention
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Pred. No. 5e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.0%;
66.7%;
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25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 802 AA;
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The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, disestive disorders (e.g. acquired disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haamatopoietic disorders, neural disorders (e.g. Alzheimer's, haamatopoietic disorders, neural disorders (e.g. Alzheimer's, seningitis, sakhison's, creutzfeldt-Jacob disease, encephalomyelitis, meningitis, and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
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                                                                                                                     New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 5; Leng...
---- No. 58+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 5e+0
1; Mismatches
                                                                                                                                                                               Claim 1; Page 1035-1037; 2102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA56848 standard; protein; 802 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2001; 2001US-0277340P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.0%;
             (HUMA.) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein #131,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                    Rosen CA, Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                786 CSVPITDPC 794
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                                                                                      WPI; 2002-010886/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 802 AA;
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The invention relates to 592 new human secreted polypeptides useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or polypeptides comprising an amino acid methodies or antibodies or antibodies or antibodies or antibodies. Sequences The polypeptides, agonists or antagonists that binds to acids encoding the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing disgnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune compositions for disgnoses, respiratory conditions [e.g. inflammatory bowel disease, disorders, inflammatory conditions [e.g. inflammatory bowel disease, allergy), cancers (e.g. gastric, ovarian or lung cancer). CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative disorders (e.g. parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The cardiovascular disorders (e.g. atherosclerosis or myocarditis). The polypuncleotides are useful for chromosome identification, chromosome mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and se hybridization corresponds to resting or preventing neural disorders, pulmonary, cardiovascular, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, in electronic format directly from NIPO at the invention, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; cancer; hyperproliferative disorder; rheumatoid arthritis; autoimmune disorder; haematopoietic disorder; anaemia; allergic reaction; asthma; cardiovascular disorder; autoimtory cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; vulnerary; cardiant; gene therapy.
                                                      New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                   Claim 13; SEQ ID NO 1038; 1754pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA40695 standard; protein; 802 AA.
                                                                                                                                         neurodegenerative disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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Matches 6; Conserv
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                   N-PSDB; ADA55952
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The invention relates to novel genes ADA3629-ADA40565 and proteins ADA40566-ADA40501 for human secreted proteins, useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene treating or ameliorating medical conditions e.g. by protein or gene fragments, and agonists or antagonists that bind to the polypeptide are diagnostic or preparing a diagnostic or parmaceutical composition for one preparing cancer or other hyperproliferative disorder. The polypeptides and mucleic acid molecules are also useful for detecting, preparing cancer or other hyperproliferative disorders including neoplasms, autoimmune crown hyperproliferative disorders including neoplasms, autoimmune crown hyperproliferative disorders including neoplasms, autoimmune crown hyperproliferative disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus canaemia, haematopoietic or haematological disorders (e.g. anaemia, chaematopoietic or haematological disorders (e.g. anaemia, chaematopoietic or haematological disorders (e.g. anaemia, chaematopoietic or parting such are cacema, inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory cromporticins adisease), neurodegenerative disorders (e.g. thepathelial cell proliferation, radiation hybrid mapping or long-consecution or diagnostic probes. The polypeptides and antibodies are consecutable or disorders of epithelial cell proliferation, radiation mapping, as molecular weight markers, or as consecution or diagnostic probes. The polypeptides and antibodies are consecuted in electronic format directly from MIPO at the printed specification, but was consecuted by examined in electronic format directly from WIPO at the printed specification, but was consecuted and reference of the printed specification, but was consecuted and reference of the printed specification.
                                                                                                                                                                                                                                                                                                                                           New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing, preventing or treating cancer or other hyperproliferative disorder, asthma, allergies or AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1077; 3205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               obtained in electronic format directly fiftp.wipo.int/pub/published_pct_sequences
                                                                          21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                           19-MAR-2002; 2002WO-US008123.
                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                        Rosen CA, Ruben SM;
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76.0%; Score 38; DB 6; Length 802; 66.7%; Pred. No. 5e+02; 1. Mismatches 2; Indels Query Match 76.0%; Best Local Similarity 66.7%; Matches 6; Conservative Sequence 802 AA; ð

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Sequence 4810, App Sequence 324, App Sequence 324, App Sequence 296, App Sequence 176, App Sequence 477, App

2 US-10-424-599-236212 6 US-10-425-114-39180 6 US-10-47-963-160508 4 US-10-106-698-4810 US-09-764-873-451 4 US-10-1158-673-451 4 US-10-1158-677-176 5 US-09-978-192A-477 1 US-09-978-477 1 US-09-978-477 1 US-09-978-477 1 US-09-978-477 1 US-09-978-477 1 US-09-98-82A-477 1 US-09-978-477 1 US-09-978-477

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Sequence 10, Appl
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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   GenCore version 5.1.6
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ALIGNMENTS

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                                                  APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: STACKER, Steven

APPLICANT: STACKER, Steven

APPLICANT: STACKER, Richard

APPLICANT: CENDEON, Angela

TITLE OF INVENTION: VEGP-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR PLING DATE: 2000-01-18

PRIOR PLING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 10

LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 50; DB 9; Length 9; 100.0%; Pred. No. 1.2e+06; cive 0; Mismatches 0; Indels
Sequence 10, Application US/09761636A; Patent No. US20020065218A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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Best Local Similarity
Matches 9; Conserv
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US-10-424-599-241613
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; Sequence 241613, Application US/10424599 ; Publication No. US20040031072A1

Sequence 206581, Sequence 174316, Sequence 205890, Sequence 69391, A Sequence 133870, Sequence 276101,

Sequence 241613, Sequence 241616,

1081, Ap 888, App 169061,

Sequence Sequence Sequence

Sequence

US-10-424-599-241613 US-10-424-599-241615 US-10-424-599-206581 US-10-424-599-105890 US-10-425-114-69391 US-10-425-114-69391 US-10-425-114-69391 US-10-425-114-599-276101 US-10-424-599-276101 US-10-424-599-169061 US-10-424-599-276082 US-10-424-599-276082 US-10-424-599-276082 US-10-424-599-276082 US-10-424-599-276082

1154 1194 1194 128 158 167 1167 215

276082, 243236, 56269, P

Sequence Sequence . 0

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Sequence 174316, Application US/10424599
; Sequence 174316, Application US/10424599
; Publication No. US20040031072A1
; GRNERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
APPLICANT: Availc David K
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5323)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174316
; LENGHIH: 359
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Palants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205890
LENGTH: 5.49
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                                                                                                                                                                                                                                           Score 41; DB 12; Length 78;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: PAT_MRT3847_128426C.1.pep
                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_28570C.1.pep
US-10-424-599-206581
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OTHER INFORMATION: ungure at all Xaa locations
FBATURE:
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, NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206581
LENGTH: 78
                                                                                                                                                                                                                                             82.0%;
66.7%;
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Matches 8; Conservative
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                1 CSVPLTSVC 9
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                                                                                                               TYPE: PRT
ORGANISM: Glycine max
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Songwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFREENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-424-599-241616
US-10-424-599-241616
Sequence 241616, Application US/10424599
Publication No. US20040031072A1
Sequence 241616, Application US/2040031072A1
Sequence 241616, Application No. US20040031072A1
SERICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21(53223)B
CURRENT RILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                  APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_60206C.1.pep
US-10-424-599-241616
                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_60203C.1.pep
US-10-424-599-241613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.8
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSSPITSVC 74
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-10-424-599-206581
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Sequence 1081, Application US/10369493

Sequence 1081, Application US/20030233675A1

Sequence 1081, Application US20030233675A1

GENERAL INPORMATION:

Sequence 1081, Application No. US20030233675A1

SEPPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Glater, Steven C.

APPLICANT: Glater, Steven C.

APPLICANT: Glater, Steven C.

APPLICANT: Glater, Manfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERIES

FILE REPERENCE: 38-10 (52052) B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 1081
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 276101, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cavalic David K
APPLICANT: Cavalic 
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                                                                                    Score 41; DB 16; Length 883;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 12; Length 63; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 432;
                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: PAT_MRT3847_91339C.1.pep
                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                                                 82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.0%;
66.7%;
                                                                                                                                               Conservative
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Matches 7; Conservative
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                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
                     US-10-437-963-133870
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US-10-369-493-1081
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APPLICANT: Li Ping
APPLICANT: Li Ping
TITLE OF INVENTION: Rice Mucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ. ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
MUMBER OF SEQ ID NOS: 73128
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Pred. No. 82;
2; Mismatches 1; Indels
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                         ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27947C.1.pep
US-10-424-599-205890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: UC-GMROPIC111B04_FLI.pep
US-10-425-114-69391
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Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: AVOILE, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.77
انمو 6; Conservative
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82 CSSPITSIC 90
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                            1 CSVPLTSVC 9
ORGANISM: Glycine max
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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Heplicant: La Rosa Thomas J

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: CANT ON YONGWei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION WNDER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 276082

TYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 243236, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: VUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 243236
LENGTH: 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_61670C.1.pep
US-10-424-599-243236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: PAT_MRT3847_91321C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.0%; Score 37; DB 12;
55.6%; Pred. No. 1.3e+02;
iive 1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.0%; Score 37; DB 12;
66.7%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(95)
OTHER INFORMATION: ungure at all Xaa locations
FEATURE:
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.0
Best Local Similarity 55.6
Matches 5; Conservative
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ORGANISM: Glycine max
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US-10-424-599-243236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: unsure
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Sequence 169061. Application US/10424599
Sequence 169061. Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(5323.8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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Pred. No. 3.9e+02;
1; Mismatches 2; Indels
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US-10-424-599-169061
                                                                                                                                                                                                                                                                     Sequence 888, Application US/0983245; Publication No. US20040010134A1; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMTION:
FILE REPREBENCE:
CURRENT APPLICATION NUMBER: US/09/833,245; CURRENT FILING DATE: 2001-04-12; PRIOR APPLICATION NUMBER: 60/229, 358 PRIOR PAPLICATION NUMBER: 60/229, 358 PRIOR FILING DATE: 2000-04-12; PRIOR APPLICATION NUMBER: 60/266, 931; PRIOR APPLICATION NUMBER: 60/199, 384 PRIOR FILING DATE: 2000-04-25; NUMBER OF SEQ ID NOS: 2267; SOFTWARE: PALENTING DATE: 2000-04-25; NUMBER OF SEQ ID NOS: 2267; SOFTWARE: PALENTING DATE: 2000-04-25; SOFTWARE: PALENTIN Ver. 2.1
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Similarity 66.7%;
6; Conservative 1
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786 CSVPITDPC 794
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                                                                                                                                                                      389 CWVPLTSFC 397
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSVPLTSVC 9
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Best Local Similarity
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LENGTH: 82
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US-09-833-245-888
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Matches
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## APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Dants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 56269
LENGTH: 215
TYPE: PRT
ORGANISM: Glycine max
FERTURE:
ORGANISM: Glycine max
FERTURE:
ORGANISM: Glycine max

CHER INFORMATION: Clone ID: 700835470_FLI.pep
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183 CSPPLTATC 191
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Query Match 86.0
Best Local Similarity 77.8
Matches 7; Conservative
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Sequence 10842, A
Sequence 20364, A
Sequence 1, Appli
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Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 4, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4725, Ap
Sequence 3, Appli
Sequence 3, Appli
                                                                          5, 2004, 09:55:30; Search time 8 Seconds (without alignments) 58.079 Million cell updates/sec
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(cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*

(cgn2_6/ptodata/2/iaa/backfiles1.pep:*
     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-252-91A-20364

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US-08-688-342-1

US-09-613-788-1

US-09-61-976-4725

US-09-61-976-4725

US-09-61-976-4725

US-09-673-395A-479

US-09-673-395A-479

US-09-673-395A-479

US-09-673-395A-479

US-09-673-395A-479

US-09-673-391A-4919

US-09-673-61A-6083

US-09-496-672-51

US-09-496-672-51

US-09-496-672-51

US-09-496-672-51

US-09-491-681

US-09-469-186-1

US-09-469-186-1

US-09-469-186-1

US-09-469-186-1

US-09-469-186-1

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US-09-469-186-1

US-09-469-186-1

US-09-469-188-8

US-08-53-246-8
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US-08-543-246B-9
US-08-543-246B-24
US-09-489-039A-13837
US-09-257-9017
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US-09-252-991A-30882
                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                   389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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                                                                                                                                        Perfect score:
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29 32 64.0 335 3 US-00-31-95-9 Sequence 9, Appli 32 64.0 335 3 US-00-31-95-9 Sequence 17.4 Appli 32 64.0 335 3 US-00-31-95-9 Sequence 17.4 Appli 32 64.0 335 4 US-00-41-95-9 Sequence 17.4 Appli 32 64.0 335 4 US-00-41-95-9 Sequence 17.4 Appli 32 64.0 336 4 US-00-41-95-9 Sequence 17.4 Appli 32 64.0 336 4 US-00-41-95-9 Sequence 17.4 Appli 32 64.0 339 1 US-00-41-95-9 Sequence 17.4 Appli 32 64.0 1431 US-00-41-95-9 Sequence 17.4 Appli 32 64.0 1431 US-00-41-95-9 Sequence 17.4 Appli 32 64.0 1431 US-00-41-95-9 Sequence 17.4 Appli 32 65.0 14 2 US-00-41-95-9 Sequence 17.4 Appli 32 65.0 14 2 US-00-491-25-5 Sequence 17.4 Appli 32 65.0 14 3 US-00-491-25-5 Sequence 17.4 Appli 32 0S-00-491-25-5 Seq
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Gaps
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GENERAL INFORMATION:

APPLICANT: Au-Young, Janice

APPLICANT: Golks, Benjamin G.

APPLICANT: Goli, Surya K.

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Forter Drive

CITY: Palo Alto
                                                                                                                                                 COPERATING SYSTEM: DOS
SOFTWARE: FASTSED VESSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,342
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELECHMONE: 415-855-0555
TELEPHAX: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.0%; Score 36; DB 66.7%; Pred. No. 63; iive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 23104
ZIP: 33104
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,788
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/688,342
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 201 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: MMLRIDT01
CLONE: 515847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-688-342-1
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US-09-113-788-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: F
STATE:
                                            COUNTRY:
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APPLICANT:

ARRUGINOSA FOR DAID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION:

ARRUGINOSA FOR DAIGNOSTICS AND THERAPEUTICS

FILE REFERENCE:

CURRENT PAPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20364
         Sequence 1042, Application US/09489039A

Sequence 1042, Application US/09489039A

Patent NO. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1099-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 10842
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Pred. No. 52;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               82.0%; Score 41; DB 4; Length 422; 100.0%; Pred. No. 19; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: AU-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goll, Surya K.
APPLICANT: Hillnan, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08688342
Patent No. 5871964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20364
                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 SVPLTSVC 394
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           US-09-489-039A-10842
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US-08-688-342-1
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APPLICANT: Abramovitz, Mark
APPLICANT: Boie, Yves
APPLICANT: Grygor-zyk, Richard
APPLICANT: Grygor-zyk, Richard
APPLICANT: Metters, Kathleen
APPLICANT: Rushmore, Thomas H.
APPLICANT: Slipetz, Deborah M.
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 4; Length 134;
Pred. No. 90;
1; Mismatches 3; Indels
                                                                                                                                                                  Sequence 4725, Application US/09621976
Fatent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Johert, S.
APPLICANT: Glordano, J.Y.
ITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 4725
LENGTH: 134

LENGTH: 134
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US-08-134-012-3
; Sequence 3, Application US/08134012
; Patent No. 551665
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OTHER INFORMATION: Xaa = Cys, Trp
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: John Wallen
126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 49,51
OTHER INFORMATION: Xaa = Ala,Gly
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 47
OTHER INFORMATION: Xaa = Gly, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa = Lys, Arg
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) LOCATION: 45
) OTHER INFORMATION: Xaa = Phe, Leu
US-09-621-976-4725
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Best Local Similarity 55.6%;
Matches 5; Conservative
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LOCATION: 52
OTHER INFORMATION: Xaa =
NAME/KEY: UNSURE
                                               293 CSIPIWKIC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                    1 CSVPLTSVC 9
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: UNSURE
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GENERAL INPORMATION:
APPLICANT: Laufer, Edward M.
APPLICANT: Orozco, Olivia E.
APPLICANT: Trabin, Clifford J.
TITLE OF INVENTION: Fringe Proteins and Pattern Formation
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
STREET: Two Millian Brook, Smith & Reynolds, P.C.
STREET: Two Millian Drive
STREET: Massachusetts
STREET: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTE: PLAIN

COMPUTE: PLADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/586,165

FILING DATE: 16-JAN-1996

CLASSIFICATION NUMBER: 32,227

REGISTRATION NUMBER: 32,227

RELECOMMUTICATION INFORMATION:

TELEFRAM: (617) 861-6240

TELEFRAM: (617) 861-6240

TELEFRAM: 359 amino acids

TYPE: amino acid

STRANDBESS: single

TYPE: amino acid

STRANDBESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-08-586-165-4
; Sequence 4, Application US/08586165
; Patent No. 6054298
                                      INFORMATION FOR SEQ 1D NO: 1: SEQUENCE CHARACTERISTICS: EMENTH: 201 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE: LIMBERAY: MALLEDTO1 CLONE: 515847
TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                187 CSVPSYSIC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSVPLTSVC 9
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LOCATION: 1..1
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                                                                                                                                                                                                                                                                                 US-09-113-788-1
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Gaps
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Sequence 3, Application US/09039798

Seneral INFORMATION:
APPLICANT: Abramovitz, Mark
APPLICANT: Grygorczyk, Richard
APPLICANT: Grygorczyk, Richard
APPLICANT: Rushmore, Thomas H.
APPLICANT: Slipetz, Deborah M.
TILE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
TILE OF INVENTION: DNA ENCODING PROSTAGLANDIN CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. Mark Hand
STREET: 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
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                                                                                                                                       Length 386;
                                                                                                                                       Query Match 68.0%; Score 34; DB 1; Length 386 Best Local Similarity 66.7%; Pred. No. 2.6e+02; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rahway
STRATE: New Jersey
COUNTRY: USA
ZIP: 07055-0907
COMPUTER READABLE FORM:
MEDLUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,519
FILING DATE: 29-AUG-1995
ATTORNEY AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 1909BDB
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 479, Application US/09673395A
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 386 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-039-798-3
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251 CSLPLTIRC 259
                                              MOLECULE TYPE: protein US-08-520-519-3
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                                                                                                                                                                                                                                                                                          1 CSVPLTSVC 9
                 TOPOLOGY: linear
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US-09-673-395A-479
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US-09-039-798-3
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APPLICANT: Boie, Yves
APPLICANT: Boie, Yves
APPLICANT: Boie, Yves
APPLICANT: Grygorczyk, Richard
APPLICANT: Grygorczyk, Richard
APPLICANT: Rushmore, Thomas H.
APPLIC
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66.7%; Pred. No. 2.6e+02;
...marrhes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rahway
STATE: New Jersey
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPBY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Version #1.25
SOFTWARE: PSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEM: PC-DOS/MS-DOS
SOFTWARE: DSTEM: DC-DOS/MS-DOS
SOFTWARE: PSTEM: DC-DOS/MS-DOS
CLASSIFICATION NUMBER: US/08/520,519
FILING DATE: 29-AUG-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TRIBDIE, Jack L.
NAME: TRIBDIE, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: 19098DA
TELECOMMUNICATION INFORMATION:
THE COMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIN Release #1.0, Version #1.25
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,012
FILING DATE: 06-COT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: WAllen, John WEBR: 35,403
REFERENCE/DOCKET NUMBER: 19098
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-520-519-3
; Sequence 3, Application US/08520519
; Patent No. 5728808
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 386 amino acids
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Best Local Similarity 66.7<sup>3</sup>
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 CSLPLTIRC 259
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US-08-134-012-3
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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GENERAL NO. 0.234423;
GENERAL INFORMATION:
APPLICANT: Takahashi, Joseph S.
APPLICANT: Turek, Fred W.
TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
TITLE REFERENCE: 0.290-5;
CURRENT APPLICATION NUMBER: US/09/496,672;
CURRENT FILING DATE: 2000-0.2-03;
PRIOR PLING DATE: 1997-06-30;
PRIOR PLING DATE: 1997-06-30;
PRIOR PLING DATE: 1997-03-13;
NUMBER OF SEQ ID NOS: 55;
SOFTWARE: PATENTIN PATE: 1997-03-13
                                                                                                                                                                                                                                                                                                                APPLICANT: Takanshi, Joseph S.
APPLICANT: Takanshi, Joseph S.
APPLICANT: Turek, Fred W.
APPLICANT: Turek, Fred W.
TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
FILE REFERENCE: 0290-5
CURRENT APPLICATION NUMBER: US/08/885,291A
CURRENT APPLICATION NUMBER: 08/816,693
EARLIER APPLICATION NUMBER: 08/816,693
SAFLIER FILING DATE: 1997-03-13
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                        US-08-885-291-51; Sequence 51, Application US/08885291A; Patent No. 6057125; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51, Application US/09496672
Patent No. 6291429
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US-09-402-016A-4
; Sequence 4, Application US/09402016A
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66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                           215 CRVPLGKVC 223
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US-08-885-291-51
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                                    CSVPLTSVC 9
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSVPLTSVC 9
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LENGTH: 747
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GENERAL INFORMATION:
APPLICANT: SPECHT THOMAS
APPLICANT: SPECHT THOMAS
APPLICANT: BEND
APPLICANT: BEND
APPLICANT: PILARSKY, CHRISTIAN
APPLICANT: BOSENTHAL, ABOMA
APPLICANT: BOSENTHAL, ABOMA
APPLICANT: BOSENTHAL, SOOR-10-17
CURRENT APPLICATION NUMBER: US/09/673,395A
CURRENT FILING DATE: 2000-10-17
SEQ ID NO 479
: LENGTH: 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Takahashi, Joseph S
APPLICANT: Turek, Fred W
APPLICANT: Turek, Fred W
APPLICANT: Pinto, Lawrence H
TITLE OF INVENTION: Clock Gene and Gene Product
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 51, Application US/08816693A
; Patent No. 5874241
; GENERAL INFORMATION:
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Best Local Similarity 85./~
".heq 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Prude
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 LPLTSVC 57
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STRANDEDNESS: siz
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Best Local Similarity
Matches 6; Conserv
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US-08-816-693A-51
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| Patent No. 6610303
| GENERAL INFORMATION:
| APPLICANT: HAUSEN, ETHEL-MICHELE DE VILLIERS-ZUR
| APPLICANT: HAUSEN, HANALD ZUR
| APPLICANT: LAVERGNE, DONNA
| APPLICANT: LAVERGNE, DONNA
| APPLICANT: BENTON, CLAIRE
| TITLE OF INVENTION: THERAPY AND VACCINATION
| FILE REPERENCE: 8484-100-999
| CURRENT APPLICATION NUMBER: US/09/402,016A
| CURRENT FILING DATE: 1998-03-24
| PRIOR FILING DATE: 1998-03-24
| NUMBER OF SEQ ID NOS: 16
| SEQ ID NO 4
| LENGTH: 126
| TENGTH: 126
| TENGTH: Papilloma virus capsid
| US-09-402-016A-4
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5.1.6	Compugen Ltd.	
e version 5.1.6	- 2004	
GenCore	(c) 1993	
	Copyright	

OM protein - protein search, using sw model

5, 2004, 09:47:29; Search time 5.37374 Seconds (without alignments) 125.302 Million cell updates/sec September Run on:

US-09-761-636A-11 42

1 CVPLTSC 7 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		1																												
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	Score	6	38	36	36	36	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	32	32	32	32	32	32
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138400	A41234	855598	T13704	T29764	S50820	T42215	508572	S16496	A33787	151295	857956	T27849	S18946	A36686	852130
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662	668	1319	2044	2180	2395	5376	63	110	120	128	146	161	169	182	190
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Surder auturation - transcrium primureting CiSpecies: Paramectium primureting CiSpecies: Paramectium primurelia CiSpecies: Paramectium primurelia CiSpecies: 19-May-2000 #sequence_revision 19-May-2000 #text_change 23-Mar-2001 CiSpecies: 19-May-2000 #sequence_revision 19-May-2000 #text_change 23-Mar-2001 CiSpecies: 0.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0010 #1.0
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92.9%; Score 39; DB 2;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches (
                  - Paramecium primaurelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Genetic code: SGC5
C;Superfamily: G surface protein
suface antigen
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## 2158 CIPITSC 2164 1 CVPLTSC 7 셤 à

7 RESULT

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(Nasonia		
D44490 retrovirus-related reverse transcriptase homolog (clone NvC) - pteromalid wasp (Nasonia C;Species: Nasonia vitripennis	C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000 C;Accession: D44490; F40442	R; Burke, W.D.; Bickbush, D.G.; Xiong, Y.; Jakubczak, J.; Eickbush, T.H.

Mol. Biol. Evol. 10, 163-185, 1993
A. Title: Sequence relationship of retrotransposable elements R1 and R2 within and betwee A; Recession: A44490, MUID: 93196484; PMID:8383793
A; Rontents: retrotransposable element R1
A; Accession: D44490
A; Returner preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-380 < LBC;
A; Molecule type: nucleic acid
A; Residues: 1-380 < LBC;
A; Molecule type: nucleic acid
A; Residues: 1-380 < LBC;
A; Residues: 20: 0.5.A; 88, 3295-3299, 1991
A; Residues: R40442; MUID: 91195337; PMID:1849649
A; Residues: preliminary; nucleic acid sequence not shown; not compared with conceptual trady. Residues: 304-320 < JAK>

0

Gaps

·.

Indels

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C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Nov-2000
C;Accession: T30886
R;Joba, W.; Hoffmann, W.
R;Joba, W.; Hoffmann, W.
A;Title: Similarities of integumentary mucin B.1 (FIM-B.1) from Xenopus laevis and prep A;Title: Similarities of integumentary mucin B.1 (FIM-B.1) from Xenopus laevis and prep A;Title: Similarities of integumentary mucin B.1 (FIM-B.1) from Xenopus laevis and prep A;Title: Similarity; translated from GB/EMBL/DDBJ A;Accession: T30886
A;Accessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Accession: A54895
R;Ohmori, H.; Dohrman, A.F.; Gallup, M.; Tsuda, T.; Kai, H.; Gum Jr., J.R.; Kim, Y.S.; J. Biol. Chem. 269, 17833-17840, 1994
A;Title: Molecular cloning of the amino-terminal region of a rat MUC 2 mucin gene homol A;Reference number: A54895; MUID:94299489; PMID:8027037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: A54895
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1513 < 0HM>
A; Cross-references: GB:U07615
C; Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; vo
C; Keywords: intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: Y08296; NID: 91839051; PIDN: CAA69604.1; PID: 91839052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mucin 2, intestinal/tracheal - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Mar_1995 #sequence_revision 23-Mar-1995 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               integumentary mucin B.1 - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X85135; NID:g728634; PID:g728635; PIDN:CAA59447.1 C;Genetics code: SGC5 A;Genetic code: SGC5 A;Note: alpha-51D C;Superfamily: G surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2533;
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71.4%; Pred. No. 1.5e+02;
iive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.0%; Score 34; DB 2; I
71.4%; Pred. No. 1.5e+02;
iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.7%; Score 36; DB 2;
57.1%; Pred. No. 98;
                                                                                                        A,Reference number: 220505
A,Reference number: 220505
A,Accession: T28674
A,Statuas: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-2533 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                      R;Schmidt, H.J.
submitted to the EMBL Data Library, March 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: pig submaxillary mucin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.45
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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2149 CIPITNC 2155
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Best Local Similarity
Matches 4; Conserv
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C; Accession: T28674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cibodextrin phosphorylase - Clostridium thermocellum Cispecies: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 15-Oct-1999 CiAccession: T00455 Tiseuchi, Y.; Tsutsumi, N.; Kan, A.; Sumitani, J.; Arai, M. T.; Kawaguchi, T.; Ikeuchi, Y.; Tsutsumi, N.; Kan, A.; Sumitani, J.; Arai, M. Title: Clonfung, nucleotide sequence, and expression of the Clostridium thermocellum Ce A; Reference number: Z14077 A; Accession: T00045 A; Accession: T00045 A; Amolecule type: DNA A; Residues: 1-980 cKAM>A; Residues: 1-980 cKAM>A; Residues: 1-980 cKAM>A; Cross-references: EMBL:AB006822; NID:d1117395; PIDN:BAA22081.1; PID:d1022940 A; Experimental source: ATCC 27405 C; Genetics: A; Gene: cdp
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C;Species: Paramecium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-51D immobilization antigen - Paramecium tetraurelia
C;Species: Paramecium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T28675
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85.7%; Score 36; DB 2; Length 2533;

Best Local Similarity 57.1%; Pred. No. 98;

Matches 4; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2; Length 980;
Pred. No. 44;
3; Mismatches 0; Indels
                                                                                    Length 380;
                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sischwegmann, K.J.

Submitted to the EMBL Data Library, March 1996
A;Reference number: 220506
A;Accession: T28675
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DMA
A;Residus: 1-2533 < SGH>
A;Residus: 1-2533 < SGH>
A;Cobs-references: EMBL:X96400; PIDN:CAA65264.1
                                                                                            DB 2;
                                                                                    Query Match 90.5%; Score 38; DB 2
Best Local Similarity 85.7%; Pred. No. 8.1;
Matches 6; Conservative 1; Mismatches
                       C; Superfamily: silkworm pol protein
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A,Genetic code: 89C5
A,Introns: 280/3; 538/2; 1248/2
C,Superfamily: G surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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2149 CIPITNC 2155
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550 CIPMTAC 556
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RiTomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 199.

A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A; Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A)Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-207 <TOM>
A;Cross-references: GB:AE000615; GB:AE000511; NID:g2314230; PIDN:AAD08133.1; PID:g23142:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein jhp0344 - Helicobacter pylori (strain J99)

C.Species: Helicobacter pylori
A,Varietr 10 J99
C.Species: Helicobacter pylori
A,Varietr 10 J99
C.Species: D.S. Helicobacter pylori
C.Species: D.S. Helicobacter pylori
C.Species: D.S. Helicopacter pylori
C.Species: D.S. Helicopacter D.S. Helicopacter D.S. Helicopacter D.S. Doing, D.S. Doi
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A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: A64655
                                                                                                                                                                       A;Residues: 1-191 <JEN>
A;Cross-references: EMBL:X73434; NID:g313719; PIDN:CAA51829.1; PID:g313720
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                   A; Reference number: I46412; MUID:94358466; PMID:7521375
                                                       A;Accession: 146412
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                   A;Gene: KRTAP5.4
C;Superfamily: ultra-high-sulfur keratin
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71.4%;
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-207 <ARN>
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CiSpecies: Sus scrofa domestica (domestic pig)
CiDate: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
CiAccession: T34022
R;Hardy, D.M.; Garbers, D.L.
B. Biol. Chem. 270, 26025-26028, 1995
A;Title: A sperm membrane protein that binds in a species-specific manner to the egg ext
A;Reference number: Z21464; MUID:96064658; PMID:7592795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Ovis orienfalis aries, Ovis ammon aries (domestic sheep)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 24-Sep-1999
C;Accession. 146412; S34215
R;Jenkins, B.J.; Powell, B.C.
J. Invest. Dermatol. 103, 310-317, 1994
A;Title: Differential expression of genes encoding a cysteine-rich keratin family in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase AK23 (EC 2.7.1.-) - Arabidopsis thaliana (fragment)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: J9-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 24-Sep-1999
C.Accession: S66336, S58262
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A,Title: Differential accumulation of the transcripts of 22 novel protein kinase genes A,Reference number: S66314; MUID:96123233; PMID:8534852
A,Accession: S6636
A,Residues: 1-55 <THU>
A,Residues: 1-55 <THU>
A,Coss-references: EMBL:X86968; NID:9928913; PIDN:CAA60531.1; PID:9928914
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A;Molecule type: mRNA
A;Residues: 1-2476 <HRR>
A;Cross-references: EMBL:U40024; NID:g1066465; PID:g1066466; PIDN:AAC48486.1
A;Experimental source: strain Meishan; testis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.6%; Score 33; DB 2; Length 55; 100.0%; Pred. No. 14; 1. Indels ive 0; Mismatches 0; Indels
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CVPLSQC 1511
                                               CVPLSKC 715
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Matches 6: Conserv
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27 CVPLTS 32
CVPLTSC
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146412
keratin KAP5.4 - sheep
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Query Match

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A; Gene: Zar C; Function

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C;Species: Musculus (house mouse)
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 24-Sep-1999
C;Accession: A38346
B;Mood, Li, Mills, M.; Hatzenbuhler, N.; Vogeli, G.
J;Biol. Chem. 265, 21375-21380, 1990
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin A;Accession: A38346, MUID:91065960; PMID:2250030
A;Accession: A38346
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                  ultra-high-sulfur keratin 2 - mouse
ultra-high-sulfur keratin 2 - mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Sep-1999
C;Accession: As8660; B8346
B;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
B;Wood, L.; Mills, M.; Hatzenbuhler, N.; Vogeli, G.
A;Title: Scrine-rich ultra high sulfur protein gene expression in murine hair and skin G.
A;Reference number: A38660; MUID:91154184; PMID:1840598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-223 <WO2>
A;Cross-references: GB:M37760; NID:g200963; PIDN:AAA40107.1; PID:g200964
A;Cross-references: GB:M37760; NID:g200963; PIDN:AAA40107.1; PID:g200964
A;Note: this is a correction
A;Note: this is a correction
J. Biol. Chem. 265, 21375-21380, 1990
A;Title: Serine-rich ultra high sulfur protein gene expression in murine hair and skin A;Reference number: A38346; MVID:91065960; PMID:2250030
A,Accession: B38346
A,Molecule type: DNA
A,Residues: 1-21, 'GGCGSGCGGSCGCKPVCC', 22-40, 'GSS', 44-45, 'G', 47-48, 'S', 50, 'GSS'
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C;Species: saimirine herpesvirus 1
A;Note: host Saimiri sciureus (common squirrel monkey)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962 A;Note: the sequence reported in this paper has been corrected. See A38660 C;Superfamily: ultra-high-sulfur keratin
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A;Cross-references: GB:M37759; NID:g200961; PIDN:AAA40106.1; PID:g200962
C;Superfamily: ultra-high-sulfur keratin
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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CVPQTAC 140
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A) Description: Primary structure of the herpesvirus saimiri genome.
A) Description: Primary structure of the herpesvirus saimiri genome.
A) Reference number: A36806
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A) A) Accession: B36808
A) A) Accession: B36808
A) Residues: 1-303 (ALB>
A) Residues: 1-303 (ALB>
A) Ross-references: GB:X64346; NID:g60320; PIDN:CA445644.1; PID:g60342
A) RAIDrecht, J. C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; W. A) Title: Primary structure of the herpesvirus saimiri genome.
A) Title: Primary structure of the herpesvirus saimiri genome.
A) Reference number: A37309; MUID:g2233688; PMID:J321287
A) Reference number: A37309; MUID:g2233688; PMID:J321287
A) Contents: annotation; possible protein-coding frames
A; Note: neither amino acid nor nucleotide sequence is given
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Pred. No. 60;
0; Mismatches 1; Indels
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C;Superfamily: varicella-zoster virus gene 35 protein
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Local Similarity 85.7%;
les 6; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Intestinal epithelium;

TISSUE=Intestinal epithelium;

X MEDINE=98180965; PubMed=9512496;

X Khatri I.A., Forstner G.G., Forstner J.F.;

"Susceptibility of the cysteine-rich N-terminal and C-terminal ends of rat intestinal mucin Muc 2 to proteolytic cleavage.";

Trat intestinal mucin Muc 2 to proteolytic cleavage.";

Eliochem. J. 331.323.30(1998).

-!- FUNCTION: Coats the epithelia of the intestines, airways, and other mucus membrane-containing organs. Thought to provide a protective, lubricating barrier against particles and infectious agents at mucosal surfaces.

-!- SUBUNIT: Multimeric.

-!- SUBCNIT: SPECIFICITY: Expressed in intestine and airway.

-!- SIMILARITY: Contains 3 VWFD domains.
                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                        MEDLINE-94299489; PubMed-8027037; Ohmori H., Gum J.R. Jr., Ohmori H., Dohrman A.F., Gallup M., Tsuda T., Kai H., Gum J.R. Jr., Chmori H., Zohrman A.F., Gallup M., Tsuda T., Kai W.S., Basbaum C.B.; Molecular cloning of the amino-terminal region of a rat MUC 2 mucin "Molecular cloning of the amino-terminal region of a rat MUC 2 mucin gene homologue. Evidence for expression in both intestine and
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Mucin 2 precursor (Intestinal mucin 2) (Fragment).
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MUCIN 2.
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PIR; A54895; A54895.
InterPro; IPR002919; TIL_Cysrich.
InterPro; IPR001007; VWF_C.
InterPro; IPR001846; VWF_D.
Pfam; PF001826; TIL; 1.
Pfam; PF00094; VWd; 3.
SMART; SM00214; VWC; 1.
SMART; SM00216; VWD; 3.
PROSITE; PS01208; VWFC_1; FALSE_NEG.
PROSITE; PS50184; VWFC_2; FALSE_NEG.
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VWFD 3.
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                                                                                 Rattus norvegicus (Rat).
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                     MEDLINE-95196971; PubMed-7890138;
Heid H.W., Schmidt A., Zimbelmann R., Schaefer S.,
Winter-Simanowski S., Stumpp S., Keith M., Figge U., Schnolzer M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell adhesion; Cytoskeleton; Structural protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                    "Cell type-specific desmosomal plaque proteins of the plakoglobin family: plakophilin 1 (band 6 protein)."; Differentiation 58:113-131(1994).
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85.7%; Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
-!- SIMILARITY: Belongs to the beta-catenin family.
-!- SIMILARITY: Contains 8 ARM repeats.
                                                28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Plakophilin 1 (Band-6-protein) (B6P).
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                                      (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                    Q28161;
28-FEB-2003 (
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MUC2\_RAT ID \_MUC2\_RAT

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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF_1; 1.
PROSITE; PS00186; EGF_2; 4.
PROSITE; PS0016; EGF_3; 1.
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS00060; MAM_2; 2.
Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAM 2.
53 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
(MUCIN-LIKE DOWAIN).
UWFD 1 (PARTIAL).
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-> V (IN REF. 1; AA SEQUENCE).

-> Y (IN REF. 1; AA SEQUENCE).

-> Y (IN REF. 1; AA SEQUENCE).

-> K (IN REF. 1; AA SEQUENCE).

A13B690375A6548C CRC64;
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EXTRACELLULAR (POTENTIAL)
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EGF-LIKE.
BX SIMILARITY.
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InterPro; IPR003328; TILa_Cysrich.
InterPro; IPR001007; VWF_C.
InterPro; IPR001846; VWF_D.
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                                                                                                                                                    InterPro; IPR006209; EGF like.
InterPro; IPR000998; MAM_domain.
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                                                                                                      EMBL; U40024; AAC48486.1; -.
PIR; T34022; T34022.
HSSP; P56682; 1CCV.
                                                                                                                                                                                                                                       Pfam; PF00008; EGF; 1
Pfam; PF00629; MAM; 2.
Pfam; PF00629; TIL; 5.
Pfam; PF00245; TIL; 5.
Pfam; PF00094; vwd; 4.
SMART; SM00137; MAM; 1.
SMART; SM00214; vwd; 2.
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203 CVPVPSC 209
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                                                  1 CVPLTSC 7
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                                                                                                                                                                                      Gene 20 protein.
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01-APR-1993
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       Query Match
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UL24 HSVSA
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                     0
                                                                                                                                                                                                                                                                                                              "Keratin associated proteins (KAPs): Characterisation of a second high
                                                                                                                                           15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
16-WAR-2014 (Rel. 43, Last annotation update)
16-WAR-2014 (Rel. 43, Last annotation update)
16-WAR-2014 associated protein 10.10)
16-WAR-2010 OR KRIAPIO.10 OR KAPIO.10.
                                                                                                                                                                                                                                                                                                                       sulfur KAP gene domain on human chromosome 21.";
J. Invest. Dermatol. 0.0-0(2003)
-! FUNCTION: In the hair cottex, hair keratin intermediate filaments are embedded in an interfilamentious matrix, consisting of hair keratin associated protein (KRTAP), which are essential for the formation of a rigid and resistant hair shaft through their extensive disulfide bond cross-linking with abundant cysteine extensive of hair keratins. The matrix proteins include the high-sulfur and high-glycine-tyrosine keratins.
-! SUBUNIT: Interacts with hair keratins.
-: TISSUE SPECIFICITY: Expressed exclusively in a narrow region of the middle portion of hair fiber cuticle.
-: SIMILARITY: Belongs to the KRTAP type 10 family.
                      Gaps
                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                 TISSUE-Scalp;
Rogers M.A., Langbein L., Winter H., Beckmann I., Praetzel S.,
Schweizer J.;
Score 34; DB 1; Length 2476; Pred. No. 92;
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A128CDBB45B74962 CRC64;
                                                                                                                        251 AA
                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ566387; CAD97467.1; -.
EMBL; AL773602; -; NOT ANNOTATED_CDS.
Genew; HGNC:22972; KRTAP10-10.
                                                                                                                        PRT;
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 81.0%;
71.4%;
                        5; Conservative
                                                                                                                        STANDARD;
                                                                   1505 CVPLSQC 1511
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104
116
1168
1168
1178
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222
221
AA,
                                                                                                                                                                                                                 Homo sapiens (Human)
   Query Match
Best Local Similarity
                                             1 CVPLTSC 7
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                                                                                                                          K10A_HUMAN
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                                                Gaps
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MEDLINE=92331688; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL24,
EHV-1 37, EBV BXRF1, HCMV UL76, ILTV ORF3, AND VZV 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=Placenta;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
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18;
Length 251;
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                                                   1; Indels
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SEQUENCE 303 Aa; 34942 MW; DF6D59F7A1C83A0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
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Last annotation update)
78.6%; Score 33; DB 1;
71.4%; Pred. No. 15;
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Last annotation update)
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                                                     Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                         Created)
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
                                Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                           STANDARD;
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Eukaryota; Metazoa;
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-!- FUNCTION: Binds in a species-specific manner to the zona pellucida of the egg. May be involved in gamete recognition and/or signaling (By similarity).

-!- SUBGNIT: Probably forms covalent oligomers (By similarity).

-!- SUBCELLUIAR LOCATION: Type I membrane protein, exclusively on the apical region of the sperm head (By similarity).

-!- DOMAIN: The MAM domains probably mediate sperm adhesion to the
                                     -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the ZIP transporter (TC 2.A.5) family.
KE4/Catsup subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zona pellucida.
DOMAIN: During sperm migration through the reproductive tracts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotā, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
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"Zonadhesin: characterization, localization, and zona pellucida
                                                                                                                                                                                                                                                                                                                                                                           Transport; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anilarity 71.4%; Score 33; DB 1; Length 515; Similarity 71.4%; Pred. No. 30; 5; Conservative 1; Mismatches 1; Indole
                    Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LINKED (GLCNAC. . .) (PC 17D7E854F4E1DAAF CRC64;
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N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC. N-LINKED (GLCNAC.
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28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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PIR; T23089; T23089.
InterPro; IPR003689; Zn.transpt_Zip.
Pfam, PF02535; Zip; 1. __transport; TransProthetical protein; Transport; TransFANSMEM. 27 47 POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21573741; PubMed=11717130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55500 MW;
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515 AA;
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386
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ZAN_RABIT
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Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Mataunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Magahari K., Masuho Y., Sasaki N.; "NEDO human cDNA sequencing project."; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                               Curr. Biol. 9:1180-1182(1999).
-!-FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation.
-!- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex (By similarity).
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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Genew, HGNC: 13582; FBXO3.

GO; GO: 00004842; F: ubiquitin conjugating enzyme activity; TAS.

GO; GO: 0006508; F: ubiquitin-protein ligase activity; TAS.

GO; GO: 0006508; P: proteolysis and peptidolysis; TAS.

InterPro; IPR001841; DUF525.

InterPro; IPR0018915; F-box.

InterPro; IPR0018915; Skp1_Skp2.
                                                                                                                   SEQUENCE OF 6-415 FROM N.A.
MEDLINE=20003061; PubMed=10531037;
Winston J.T., Koepp D.M., Zhu C., Elledge S.J., Harper J.W.;
"A family of mammalian F-box proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 1; Length 471;
Pred. No. 28;
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ASP/GLU-RICH (HIGHLY ACIDIC)
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EM -> VS (IN REF. 2).
F7AA88193E14E67E CRC64;
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15-MAR-2004 (Rel. 43, Last amnotation update)
Hypothetical Ke4-like protein H13N06.5 in chromosome X.
H13N06.5.
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54590 MW;
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71.48;
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Pfam; PF00646; F-box; 1.
SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; 1
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DOMAIN 10 56
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193 CLPLTFC 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50060; MAM_2; 2.
Glycoprotein; Transmembrane; EGP-like domain; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248290 MW; 380FA81093454892 CRC64;
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CYTOPLASMIC (POTENTIAL)
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VWFD 1 (TRUNCATED).
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Interpro; IPR000542; EGF 2.
Interpro; IPR000509; EGF like.
Interpro; IPR0005919; INL Cysrich.
Interpro; IPR0019019; TIL Cysrich.
Interpro; IPR001907; VWF C.
Interpro; IPR001004; VWF D.
PÉan; PF00008; EGF; 1.
PÉan; PF00008; EGF; 1.
PÉan; PF00008; EGF; 1.
PÉan; PF0008; ILL; 5.
Péan; PF00049; VWF, 2.
Péan; PR00134; VWC; 2.
SWART; SW00114; VWC; 2.
                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF 2; 4.
PROSITE; PS0026; EGF 3; 1.
PROSITE; PS00740; MAM 1; FALSE_NEG.
PROSITE; PS50060; MAM 2; 2.
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VWFD 4
VWFD 5
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HSSP; P56682; 1CCV.
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78.6%; Score 33; DB 1; Length 2282;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteolysis.
-!- SIMILARITY: TO MAMMALIAN VON WILLEBRAND FACTOR.
-!- SIMILARITY: THE N-TERMINAL DOMAIN SHOWS SOME SIMILARITY TO THAT
OF HUMAN WUCIN 2.
-!- SIMILARITY: Contains 2 F5/8 type C domains.
-!- SIMILARITY: Contains 2 VWFC domains.
-!- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kotani E., Yamakawa M., Iwamoto S.-I., Tashiro M., Mori H., Sumida M., Matsubara F., Taniai K., Kadono-Okuda K., Kato Y., Mori H.; "Cloning and expression of the gene of hemocytin, an insect humoral lectin which is homologous with the mammalian von Willebrand
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2221-3133 FROM N.A.

Kotani E., Iwamoto S.I., Tashiro M., Mori H., Sumida M.,

Matsubara F., Yamakawa M.;

Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Adhesive protein and relates to hemostasis or encapsulation of foreign substances for self-defense.

-!- DEVELOPMENTAL STAGE: Expressed in hemocytes during larVal-pupal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metamorphosis.
-!-INDUCTION: Hemagglutination activity is increased by bacterial or viral infection and inhibited by D-mannose, N-acetyl-D-galactosamine and D-maltose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: May be converted into the 260 kDa mature hemocytin by
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                         01-FFB-1996 (Rel. 33, Created)
01-FFB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hamcoytin precursor (Humoral lectin).
                                                                                                                                                                                                        PRT; 3133 AA
                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Fuyou X Tokai; TISSUE=Hemocyte;
MEDLINE=95178544; PubMed=7873598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006207, Cys knot_C.
InterPro; IPR000421; FA58 C.
InterPro; IPR009199; Gal_Bind_like.
InterPro; IPR022172; LDL_receptor_A.
InterPro; IPR02219; TIL_Cysrich.
InterPro; IPR001007; WWF_C.
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Pfam; PP00754; F5 F8 type_C; 2.
Pfam; PP01826; III; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D29738; BAA06160.1; -. EMBL; D14035; BAA03124.1; -. PIR; S52093; S52093. HSSP; P12259; 1CZT.
                                       5; Conservative
                                                                                                               1316 CVPLNOC 1322
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NCBI_TaxID=7091;
               Best Local Similarity
Matches 5; Conserv
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Pfam; PF00094; vwd; 3.

SMART; SM00231; FASBC; 2.

SMART; SM00231; FASBC; 2.

SMART; SM00216; VWD; 3.

PROSITE; PS01185; CTCK 1; 1.

PROSITE; PS01285; CTCK 2; 1.

PROSITE; PS01285; FASBC 1; 2.

PROSITE; PS01286; FASBC 1; 2.

PROSITE; PS01286; FASBC 2; 2.

PROSITE; PS01208; VMFC 1; FALSE NEG.

Lectin; Glycoprotein; Signal; Repeat; Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW; E5210D5D14A7B2B2 CRC64;
                                                                                                                                               C-TYPE LECTIN (ATYPICAL).
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BY SIMILARITY.
N-LINKED (GLCM)
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F5/8 TYPE C
                                                                                POTENTIAL.
                                                                                        HEMOCYTIN
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POLY-PRO.
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Score 33; DB 1; Length 3133; Pred. No. 1.9e+02;

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If and polymorphism.";

I. Clin. Invest. 88:1005-1013(1991).

I. FUNCTION: Coasts the epithelia of the intestines, airways, and other mucus membrane-containing organs. Thought to provide a protective, lubricating barrier against particles and infectious gants at mucosal surfaces.

I. SUBGUNIT: Multimeric.

I. SUBCELTURAR LOCATION: Secreted.

I. SUBCELTURAR LOCATION: Secreted.

INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).

INTERCHAIN STATE INTERCHAIN 1C - terminal cystine knot-like (CTCK) domain.

III (Trypsin inhibitory-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstream and downstream of its central repetitive region."; J. Biol. Chem. 267:21375-21383(1992).
          Gaps
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MEDLINE-94132002; PubMed=8300571;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.;
"Molecular cloning of human intestinal mucin (MCC2) cDNA.
Identification of the amino terminus and overall sequence similarity to prepro-von Willebrand factor.",
J. Biol. Chem. 269:2440-2446(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1343-1895 AND 4176-4195 FROM N.A. MEDLINE=91358717; PubMed=1885763; Toribara N.W., Gun J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W., Petersen G.M., Kim Y.S., "MUC-2 human small intestinal mucin gene structure. Repeated arrays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gum J.R. Jr., Hicks J.W., Toribara N.W., Rothe E.-M., Lagace R.E., Kim Y.S.;
                                                                                                                                                                                                                                                                                                                                    Dukaryota, Medazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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        Indels
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01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
02-NOV-1997 (Rel. 41, Last annotation update)
Mucin 2 precursor (Intestinal mucin 2).
MUCZ OR SMUC.
Homo sapiens (Human).
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    Mismatches
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MEDLINE=93016075; PubMed=1400449;
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EMBL; M74027; AAAS9875.1; -.
EMBL; M94131; AAAS9163.1; -.
  5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-96424990; PubMed-8827441;
MEDINE-96424990; PubMed-8827441;
MACHAINE-96424990; PubMed-8827441;
MACHAINE, Hayashi K., Takano R., Nakazawa H., Mori H., Ichida M.,
MACHAINE, Hayashi K., Hara S.;
Tapression of Bombyz family fungal protease inhibitor F from Bombyz
mori by baculovirus vector.";
J. Biochem. 119:1080-1085(1996).
M. 2)
M. 2)
M. 2)
M. 2)
M. 3
M. 3
M. 4
M. 7
M. 115SUE-Fat body;
M. 6
M. 7
MARAINE-C124; TISSUE-Fat body;
M. 1
M. 7
MACHAINE-C124; TISSUE-Fat body;
M. 1
M. 7
MACHAINE-C124; TISSUE-Fat body;
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M. 1
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01-NOV-1997 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Fungal procease inhibitor F precursor (FPI-F).
Bombyx mori (Silk moth).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera; Endoperygota; Lepidoptera; Glossata; Dirrysia; Bombycoidea;
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          (POTENTIAL).
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Pred. No. 3.1e+02;
0; Mismatches 2; Indels
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NCBI_TaxID=7091;
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InterPro; IPR006208; Cys Knot.
InterPro; IPR006209; Cys Knot.
InterPro; IPR006209; Egg=Knot.
InterPro; IPR006209; Egg=Inter-
InterPro; IPR001097; VWF_C.
InterPro; IPR001097; VWF_C.
InterPro; IPR001091; VWF_D.
Pfam; PF000097; VWC; I.
Pfam; PF000094; VWC; I.
Pfam; PF000994; VWC; I.
Pfam; PR00126; VWC; I.
PR0SITE; PS01185; CTCK_I; I.
PROSITE; PS01185; CTCK_I; I.
PROSITE; PS01205; VWFC_I; I.
PROSITE; PS01205; VWFC_I; I.
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SIGNAL 1 20
CHAIN 21 5179
       EMBL; M94132; AAA59164.1;
PIR; A49963; A43932.
Genew; HGNC:7512; MUC2.
MIM; 158370; -.
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Pfam; PF00097; zf-C3HC4; 1.

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01-MAR-1992 (Rel. 21, Created)

01-MAR-1992 (Rel. 21, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Peroxisome assembly factor-1 (PAF-1) (Peroxin-2) (Peroxisomal membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE=94309666; PubMed=8035823;
TSUKRAMOTO T., Shimozawa N., Fujiki Y.;
"Percoxisome assembly factor 1: nonsense mutation in a peroxisome-sassembly factor 1: nonsense mutation in a peroxisome-deficient Chinese hamster overy cell mutant and deletion analysis.";
Mol. Cell. Biol. 14:5458-5465(1994).
-!- FUNCTION: Somewhat implicated in the biogenesis of peroxisomes.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Peroxisomal.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91163637, PubMed=1750930,
Tratkannor T., Miura S., Fujiki Y.;
TRESTORATION by a 35K membrane protein of peroxisome assembly in a
peroxisome-deficient mammalian cell mutant.";
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                                                                                                                                                                                                                                                                                                                                                            8492 MW; B9CFC085DDA10354 CRC64;
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                                                                                                                                                                 POTENTIAL.
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EMBL; D30616; BAA06306.1; -.
EMBL; D30617; BAA06307.1; -.
IR; B53782; B53782.
InterPro; IPR006845; Pex2 Pex12.
InterPro; IPR001841; Znf ring.
Pfam; PF04757; Pex2_Pex12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PXMP3 OR PEX2 OR PAF1 OR PMP35.
                            EMBL; S83181; AAB46908.1; -.
EMBL; D38075; BAA22409.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                76.2%;
57.1%;
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                                                                            PIR; JC4790; JC4790.
InterPro; IPR002919;
Serine protease inhib
SIGNAL 1
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77 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                 Length 305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 379;
                                                                                                                                                                                                                                                                                                                                   0; Indels
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125 125 R -> P.
305 AA; 34767 MW; 249058A5A5A8EB54 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Development 120:1601-1611(1994).
-!- SIMILARITY: Contains 3 prespore motif repeats.
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83.3%; Pred. No. 28;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
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                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                  SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
Transmembrane; Peroxisome; Zinc-finger.
                                                                                                                                POTENTIAL
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Pred. No. 3
                                                                                                                                                     POTENTIAL
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57.1%;
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Best Local Similarity 83.33,
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InterPro; IPR003645; Foln.
SMART; SM00274; FOLN; 1.
Glycoprotein; Repeat; Sporul
SIGNAL
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RESULT 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                   "The CDNA RPEL and monoclonal antibody HWB-50 define gene products whe cDNA RPEL and monoclonal pigment epithelium.";

Exp. Eye Res. 55:657-662(1992).
-!- FUNCTION: Could be a melanogenic enzyme (By similarity).
-!- FUNCTION: Could be a melanogenic enzyme (By similarity).
-!- TISSUE SPECIFICITY: Retinal pigment epithelium.
-!- TISSUE SPECIFICITY: Retinal pigment epithelium.
-!- SIMILARITY: BELONGS TO THE PMEL-17/NMB FAMILY.
-!- SIMILARITY: Contains 1 PKD domain.
                                                                                                                                      Bos taurus (Bovine).
Eukaryota, Metazooa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea,
Bovidae; Bovinae, Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X 13 AA APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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0
                                                        01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Melanocyte protein Pumel 17 (Retinal pigment epithelial-specific protein) (Fragment).
SILV OR PMELL 7 OR RPEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M81193; AAA30419.1; -. PIR; A49179; AAA30419.1; -. PIR; A49179; AA9179. PED.; PED.000001; PKD. PED.000009; PKD.1. PEO.00009; PKD; 1. PROSITE; PS50093; PKD; 1. PROSITE; PS50093; PKD; 1. TRAISEmembrane; Glycoprotein; Melanin biosynthesis; Repeat. TRAISEMEM 424 444 POTENTIAL. CTODMAIN 425 491 CYTOPLASMIC (POTENTIAL). PONAIN 60 DOMAIN 148 256 8 X 13 AA APPROXIMATE TANDEM REPERENTED. PKD. 150 DOMAIN 148 160 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.2%; Score 32; DB 1; Length 491; 83.3%; Pred. No. 46; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZBBFESDFBD397D6D CRC64;
              491 AA.
              PRT;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Retina;
MEDLINE-93122163; PubMed=1478275;
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                                            (Rel. 35, Created)
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Matches 5; Conservative
              STANDARD;
                                                                                                                                                                                                                                                                              Kim R.Y., Wistow G.J.;
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1161
1174
1187
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2232
244
269
396
491 AA;
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                                              01-NOV-1997
                 PM17 BOVIN
Q06154;
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CARBOHYD
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Search completed: September 5, 2004, 09:56:08 Job time : 4.18182 secs

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2 VPLTSC 7

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mus muscult

Q9xsv8 bos taurus Q8spm4 bos taurus

Q8iya6 1 Q9xsv8 1

Quanto Coccuta cro
P19927 xenopus lae
P19927 xenopus lae
Queest homo sapien
Quiug9 komo sapien
Quiug0 komo sapien

Q92m78 helicobacte Q6220 mus musculu Q64507 mus musculu Q61ku4 sorghum bic Q7vgx3 helicobacte Q92858 saimiriine Q40640 saimiriine Q91vi9 mus musculu

musculu

Q9jie4 mus 296q28 homo

28bzi8 mus musculu

09d226 mus musculu 025713 helicobacte

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

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RP MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., In P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.W., Banco P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burks K.C., Eusam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Burks K.C., Eusam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Geblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Burkis N.C., Rangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopiera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     575 AA.
                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                           Q8M1K0
P79927
                                                                Q8TESI
Q8WWQ8
Q8WWQ8
Q7ZSN9
Q9YGR7
Q38989
Q91898
Q96BWZ
Q96BWZ
Q96BWZ
Q96BWZ
Q96BWZ
Q96Z2
Q86BWZ
Q96Z2
Q64S07
Q90G4Q
 Q7TN57
Q8IYA6
Q9XSV8
Q8SPM4
                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Q8BZJ8
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Eukaryota; Metazoa; Arthropoda; Hexi
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 685
745
1637
5146
912
1506
1736
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101
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207
207
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8833.3
8833.3
8833.3
8811.0
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 CG32260.
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QSIRBS
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O9gmw9 macaca fasc
Q833X0 enterococcu
Q18464 herdmania m
O24780 clostridium
P90589 paramecium
Q27183 paramecium
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Q90993 gallus gall
Q823i4 chlamydophi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9cxm8 mus musculu
Q8tf36 homo sapien
Q8n8u9 homo sapien
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                                                               September 5, 2004, 09:46:09; Search time 15.8384 Seconds (without alignments) 139.448 Million cell updates/sec
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                                                                                                                                                                                                               1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                     1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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P90589
Q27183
Q8CG65
Q90993
Q82314
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P90649
Q9GMW9
Q833X0
O18464
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Gapop 10.0 , Gapext 0.5
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QBTF36
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QBCJ69
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sp_mammal:*
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sp_unclassified:*
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sp_bacteriap:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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1127
1273
3374
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2533
4998
465
465
685
685
                                                                                                                               1 CVPLTSC 7
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Score

Result Š 200400400400

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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L., RA Nelson D.E., RA Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M., Raese M.G., Palazzolo M., Pittwan G.S., Pan S., Pollard J., Puri V., Reese M.G., Sahener K., Sden-Kiamos I., Simpson M., Strong R., Shen H., She B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E., Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X., A Williams S.M., Woodager, Worley K.C., Wu D., Yang S.K., Tector C., Turner R., Venter E., Wang A.H., Wang X., A Williams S.M., Woodager, Worley K.C., Wu D., Yang S. Kao Q.A., Ye J., A Yeh R.F., Zaveri J.S., Zhan M., Zhong W., Zhou X., Zhu S., Zhu S., Myers B.W., Wooley E.W., Venter J.C.;

A Gibbs R.A., Myers B.W., Woolley K.C., Wu D., Yang S., Zhu X., Smith H.O., R. Ching R., Myers B.W., Wolley R., Wolley R., Shu K., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., R. Cience 287:2165-2195 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Celniker S.E., Adams M.D., Amanatides P.C., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Libegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

Andintosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Rhouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

By Strong R., Svireks R., Tector C., Tyler D.,

Stapleron M., Strong R., Svireks R., Tector C., Tyler D.,

Stapleron M., Strong R., Swireks R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of Drosophila melanogaster genome ",

Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Matthews B.B., Bayraktaroglu L., Campbell K., Matara S., Crosby M.A., Matthews B.B., Prochnik S.E., Smith C.D., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.9%; Score 39; DB 5; Length 575; llarity 85.7%; Pred. No. 6.3; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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FlyBase; FBGN052260; CG32260.

GO; GO:0004263; F:chymotrypain activity; IEA.

GO; GO:0004256; F:crypain activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR006604; CLIP.

InterPro; IPR00154; Peptidase 51.

InterPro; IPR001254; Peptidase 51.
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SMART; SMO0680; CLIP; 1.
SMART; SMO0020; TRYP_SPC; 1.
PROSITE; PSSO240; TRYPSIN DOM; 1.
PROSITE; PSO0135; TRYPSIN_SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bourgain-Guglielmetti F., Caron; "Molecular characterization of the D surface protein gene subfamily in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Macaca fascicularis (Crab eating macaque) (Cynonigus monkey).
Malexaryotas, Metazod, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                              Paramecium primaŭrelia.
Eukaryota, Alveolata; Ciliophora; Oligohymenophorea, Peniculida;
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BMBL, AB047606, BAB12130.1; -.
Hypothetical protein.
SEQUENCE 127, AA; 12961 MW; EE168525256992CO CRC64;
                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.5%; Score 38; DB 6;
85.7%; Pred. No. 2.8;
tive 1; Mismatches
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                                                                                                                                                                         PRT; 2543 AA.
                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96313351; PubMed=8768434;
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TrEMBLrel. 03, I
(TrEMBLrel. 24, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 71.7.
Since Since Conservative
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                                                                                                                                                                                                                       01-MAY-1997 (TrEMBLrel.
01-MAY-1997 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2158 CIPITSC 2164
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204 CLPLTSC 210
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Best Local Similarity
                                                                                                                                                                                                                                                                                                             156D suface antigen.
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CVPLTSC 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  libraries.";
                                                                                                                                                                                                                                                                                                                                                                                         Paramecium.
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                                                                                                                                                                                                       P90649;
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                                                                                                                                 RESULT
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Length 337;

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STRAIN=ATC27405;
Kawaguchi T., Ikeuchi Y., Tsutsumi N., Kan A., Sumitani J., Arai M.;
"Cloning, nuclectide sequence, and expression of the Clostridium
thermocallum cellodextrin phosphorylase gene and its application to
J. Ferment. Bioeng. 85:144-149(1998).
EMBL; AB006822; BAA22081.1; -.
PIR; T00045; T00045.
InterPro; IPR008928; Glyco trans 6hp.
SEQUENCE 980 AA; 111183 WW; BARC8EB3F5370831 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paramecium tetraurelia.
Eukaryota, Alveolata, Ciliophora, Oligohymenophorea, Peniculida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.7%; Score 36; DB 2; Length 980; 57.1%; Pred. No. 42; cive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X96400; CAA65264.1; -.
PIR; T28675; T28675.
LINTEXPLO; IPR002895; Paramecium SA.
Pfam; PF01508; Paramecium SA; 21.
SMART; SM00639; PSA; 26.
SEQUENCE 2533 AA; 264142 MW; EAED7F21E408C371 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwegmann K., Klein H., Schmidt H.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                         UNKNOWN PROTEIN.
; 5CCA0924118D8FC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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01-MAY-1997 (TYEMBLrel. 03, Last sequence update)
01-UNY-2003 (TYEMBLrel. 24, Last annotation update)
Alpha-51D immobilization antigen.
                                                                                            B5.7%; Score 36; DB 5; 71.4%; Pred. No. 17; Live 2; Mismatches
                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                               Created)
                                                          35617 MW;
Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2003 (TrEMBLrel. 25, Cellodextrin phosphorylase.
                                                                        Ouery Match
Best Local Similarity 71.*.
5; Conservative
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Best Local Similarity 57.1-
---- 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium thermocellum
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                     18
                                       337
                                                                                                                                                                                              199 CVPISSC 205
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                           SIGNAL 1
CHAIN 19
SEQUENCE 337 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1515;
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                                                                                                                                                                                                                                                                                                                          024780;
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P90589
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STRAIN=VS83 / ATCC 700802;
MEDLINE=22550857; Pubmed=12663927;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Bisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
"Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                            Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCB_TaxID=1351;
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"A novel gene containing multiple EGF-like motifs transiently expressed in the papillae of the ascidian tadpole larvae.";
EMBL, U82540; AAB67704.1; -.
InterPro: IPR006210; IEGF.
InterPro: IPR002919; TIL_Cysrich.
SMART; SM00181; EGF; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
Local Similarity 71.4%; Pred. No. 17;
es 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68456 MW; 4940914DE5174E0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Herdmania.
                                                            Q833X0,
Q833X0;
Q833X0;
Q833X0;
Q8.3X0;
Q8.3X03 (TEMBLrel. 24, Created)
Q1-JUN-2003 (TEMBLrel. 24, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Glycosyl hydrolase, family 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:000341; C:beta-galactosidase complex; IEA. GO; GO:0004565; F:beta-galactosidase activity; IEA. GO; GO:0016787; F:bydrolase activity; IEA. GO; GO:0016787; F:bydrolase activity; IEA. GO; GO:0016787; F:bydrolase metabolism; IEA. InterPro; IPR001944; Glyco_hydro_35. FEAM: FROI301; Glyco_hydro_35; I. FRINTS; PR00742; GLHYDRIASE35. Hydrolase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecalis.";
Science 299:2071-2074(2003).
EMBL; AE016952; AAO81573.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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TIGR;

RESULT 4
20833X0
D0833X0
D1-U1-U1
DT 01-U1
DT 01-U1
DE G19C
GN EF18
ON EF18
CN NCBI
RR FRA PAUI
RRA CON
RRA

018464;

RESULT 5
018464
01864
AC 01844
AC 01842
DT 01-J
DT 01-J
DT 01-J
DT 01-G
DE HYPC
GN HMEC
OC BUK
OC BU

018464

Matches

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PRT;
Cys_knot_C.
EGF_like.
                                                                                                                                                                                                    PRINTS; PR00261; LDLRECEPTOR
PRINTS; PR01705; TSP1REPEAT.
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nes 5; Conservative
                                                                                                                                                                                                                           SMART; SM00192; LDLa; 10.
SMART; SM00209; TSP1; 25.
SMART; SM00214; VWC; 4.
SMART; SM00215; VWC out; 9.
SMART; SM00216; VWD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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             InterPro;
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Matches
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Q90993
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                                        Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A GONCALDER, TISSUE-Brain,
A GONCALVER, Simon-Chazottes D., Creveaux I., Meiniel A.,
Guenet J.L., Meiniel R.; Simon-Chazottes D., Creveaux I., Meiniel A.,
Guenet J.L., Meiniel R.; Simon-Chazottes B., Creveaux I., Meiniel A.,
Guenet J.L., Meiniel R.; Simon-Chazottes B., Characterization, spatio-temporal expression and chromosomal
T assignment of mouse SCO-spondin.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
E EMBL; AJ491857; CAD4554.1;
R GO; GO:0005507; C:0xtracellular; IEA.
R GO; GO:0005507; F:copper ion binding; IEA.
R GO; GO:0005179; F:hormone activity; IEA.
R GO; GO:0005179; F:hormone activity; IEA.
R GO; GO:0005179; F:hormone activity; IEA.
R GO; GO:0005189; P:electron transport; IEA.
R GO; GO:000518; P:electron transport; IEA.
InterPro; IPR000923; BlueCu_1.
                                                                                                                                                                                                                     Paramecium tetraurelia.
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
Paramecium.
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85.7%; Score 36; DB 5; Length 2533;

Best Local Similarity 57.1%; Pred. No. 96;

Matches 4; Conservative 3; Mismatches 0; Indels
                DB 5; Length 2533;
                                                                                                                                                                                                                                                                                                     STRAIN=51;
Schmidt H.J.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X88135; CAA59447.1; -.
PIR; T28674; T28674; T28674; T28674; T28674; T28674; Prop. IPR002895; Paramecium SA.
Pfam; PR01508; Paramecium SA.
Pfam; PR01508; Paramecium SA.
SMART; SM00639; PSA; 26.
SEQUENCE 2533 AA; 263996 MW; 261BD09806BC344D CRC64;
                                        0; Indels
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Last annotation update)
                                                                                                                                                            Q27183;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Alpha-51D-immobilization antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 4998 AA.
                Score 36; DB 5
Pred. No. 96;
3; Mismatches
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QBCG65,
QBCG65,
QBCG65,
QBCG65,
QBCG72003 (TERMELrel. 23, La
QBCG7-2003 (TERMELrel. 23, La
SCO-spondin.
SCO-spondin.
                 Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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2149 CIPITNC 2155
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2149 CIPITNC 2155
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Q27183
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ID Q8
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TISSUB-Peccoralis muscle;
MEDLINE=90318371; PubMed=2115117;
MEDLINE=90318371; PubMed=2115117;
Dorai T., Mang L.-H.;
"An alternative non-tyrosine protein kinase product of the c-src gene in chicken skeletal muscle.";
Mol. Cell. Biol. 10:4068-4079(1990).
-- SIMILARITY: CONTAINS 1 SH3 DOWAIN.
EMBL, M57290; AAAAONTAINS 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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PROSITE; PS0125; CTCK 2; 1.

PROSITE; PS0186; EGF 2; 2.

PROSITE; PS0186; EGF 3; 1.

PROSITE; PS01261; GLXCO_HORMONE_BETA_1; 2.

PROSITE; PS01209; LDLRA_1; 8.

PROSITE; PS01209; LDLRA_2; 10.

PROSITE; PS01209; TSP1; 25.

PROSITE; PS01209; WFC 2; 1.

PROSITE; PS01209; WFC 2; 1.

PROSITE; PS01209; WFC 2; 2.

PROSITE; PS01209; WFC 2; 2.

SEQUENCE 4999 AA; 535019 WW; DAZABABDA47DF225 CRC64;
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71.4%; Pred. No. 1.7e+02;
iive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P00523; 1SRL.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
Interpro; IPR000980; SH2.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
InterPro; 1PR0005209; ESF LIKE.
InterPro; 1PR0005421; ESF LIKE.
InterPro; 1PR001545; Gly_hormoneB.
InterPro; 1PR001572; LDL_receptor_A.
InterPro; 1PR000814; TSP 1.
InterPro; 1PR000884; TSP 1.
InterPro; 1PR000885; TSP 1.
InterPro; 1PR001087; VWF D.
InterPro; 1PR00107; VWF D.
InterPro; IPR00107; VWF D.
InterPro; IPR00157; UNF D.
Pfam; PF00757; Idl_recept_a; 10.
Pfam; PF00095; TIL, 10.
Pfam; PF00099; VWG; 1.
Pfam; PF00099; VWG; 1.
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RX MEDLINE=21085660; PubMed=11217851;
RX MEDLINE=21085660; PubMed=11217851;
RA Arakawa T., Hara A., Fukunishi Y., Konno M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Isaawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Saro K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wilttaker C., Wilming L.,
RA Hayashizaki Y.,
RY "Punctional annotation of a full-length mouse cDNA collection.",
                                                                                                                    FEQUENCE FROM N.A.

TISSUB-subcommissural organ;

MEDLINE-9822846; PubMed=5560467;

Nualart F., Hein S., Yulis C.R., Zarraga A.M., Araya A.,

Rodriguez E.M.;

Partial sequencing of Reissner's fiber glycoprotein I (RF-Gly I).";

Cell Tissue Res. 292:239-250 (1998).

EMBL; AF078930; AAD17695.1; -...
                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 389;
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SEQUENCE 389 AA; 40720 MW; 48571E1F16F9F1B6 CRC64;
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Last annotation update)
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71.4%; Pred. No. 31;
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Pfam; PF01885; TIL; 1.
Pfam; PF00190; tSpI.; 1.
SMART; SM00209; TSPI.; 1.
PROSITE; PS00261; GLYCO HORMONE_BETA_1; 1.
PROSITE; PS50092; TSPI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                     GO, GO:0005576; C:extracellular; IEA.
GO; GO:0005179; F:hormone activity; IEA.
InterPro; IPR001545; GIY hormoneB.
InterPro; IPR002919; TIL Cysrich.
InterPro; IPR000884; TSPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last seq 01-JUN-2003 (TrEMBLrel. 24, Last ann 3110056H04Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Mus musculus (Mouse)
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les 5; Conserv
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Q9CXM8
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MEDLINE=22569155; PubMed=12682364;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPIC):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC); examining the role of niche-specific genes in the evolution of the Chlamydiaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83557;
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                                                                                                                                                                                                                                                                                                                   Length 193;
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                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                  9D1BE54C33B02D98 CRC64;
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InterPro; IPR002589; Alpp.
SMART; SM00506; Alpp; 1.
Hypothetical protein; Complete protecme.
SBQUENCE 379 AA; 40634 MW; 62879277DBADD55D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Reissner's fiber glycoprotein I (Fragment).
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                            83.3%; Score 35; DB 13; 71.4%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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EMBL; AE016995; AAP05172.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                              193 AA; 21180 MW;
           Pfan; PP00017; SH2; 1.
Pfan; PP00018; SH3; 1.
PRINTS; PR00401; SH3DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000093; SH2; 1.
SWART; SW00252; SH3; 1.
SWART; SW00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                ilarity 71.4%;
Conservative
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InterPro; IPR001452; SH3.
                                                                                                                                                                                           PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SH3 domain.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
CCA00426
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Query Match

Matches

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097887; 097887 RESULT 12 097887 ID 09788 AC 09788 DT 01-MA DT 01-MA DT 01-JU DE REISSI OS BOS LI

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NCBI_TaxID=9606;
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       RESULT 15
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RA MEDELINE-21842142; PubMed=11853319;

RA Nagase T., Kikuno R., Ohara O.;

RA Nagase T., Kikuno R., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XXII.

The complete sequences of 50 new cDNA clones which code for large

RT The complete sequences of 50 new cDNA clones which code for large

RT BEBL; AB075845; BAB85551.1; -

DR GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005599; F:calcium ion binding; IEA.

R GO; GO:0005599; F:calcium ion binding; IEA.

DR InterPro; IPR000291; VIEZ dep_GLA.

DR InterPro; IPR001846; VWF_D.

DR Pfam; PF00093; vwc; 3.

DR Pfam; PF00093; vwc; 3.

DR SMART; SM00216; VWD; 1.

DR SMART; SM00216; VWD; 1.

DR PROSITE; PS000118; VWPC_1; 2.

DR PROSITE; PS010184; VWPC_2; 2.

RM MPOCHELICAL PTOTE: PTOT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                         Query Match

83.3%; Score 35; DB 11; Length 462;
Best Local Similarity 71.4%; Pred. No. 36;
Matches 5; Conservative 2; Mismatches 0; Indels
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SEQÜENCE 565 AA; 62934 MW; 1F7A15206F2B9D45 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QRTP16;
01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein KIAA1965 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565 AA
               HSSP; PO0214; IFTC.
MDD; MGI:1920480; Cv2.
InterPro; IPR002919; TIL Cysrich.
InterPro; IPR001007; VWF C.
InterPro; IPR001846; VWF C.
InterPro; IPR001846; VWF C.
Ffam; PF001826; TIL; 1.
Ffam; PF00093; vwc; 2.
Ffam; PF00093; vwc; 2.
SWART; SM00214; VWC; 2.
SWART; SM00216; VWF 1.
PROSITE; PS01208; VWF 1; 1.
PROSITE; PS01208; VWF 1; 1.
SEQUENCE 462 AA; 51641 MW; 5867
EMBL; AK014221; BAB29213.1;
HSSP; P00214; 1FTC.
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Best Local Similarity 57.1.
Local 4; Conservative
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Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamancto J., Isono Y., Kawai-Hio Y., Satro K., Nishikawa T., Kimura K., Yamashira H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Kanehori K., Sugano S., Nagahari K., Masuko Y., Nagai K., Isogai T., Nabo human cDNA sequencing project.";
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Beinerts M.E., Wen X., Cante-Barrett K., Bright J., Chen H.-T.,
Beinnerts M.E., Wen X., Cante-Barrett K., Bright J., Chen H.-T.,
Agundi V., Sattari P., Tang T., Boyle B., Funk W., Rupp F.;
Laubmitted (JUN-2013) to the EMBL/GenBank/DDBJ databases.

Benel, ANG96150; BACG4712.1; -
BENEL, ANG96150; BACG4712.1; -
BENEL, ANG96150; AAP89012.1; -
BENEL, ANG9550; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

RO; GO:0005576; C:extracellular; IEA.

RO; GO:0005579; F:calcium; ion binding; IEA.

InterPro; IPR000294; VILE Gyrich.

RITHERPO; IPR00194; VWF_D.

REAM: PR00093; VWC; 3.

REAM: SMOART; SM00214; VWC; 3.

REAM: SMOART; SM00214; VWC; 2.

REAMERT; SM00214; VWC; 2.

REAMERT; SM00216; VWF_C.

REAMERT; SM00216; VWFC_C.

REAMERT SM00216; V
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE 685 Aa; 75996 MW; A5048AADEBF04ABO CRC64;
                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ38831 (Crossveinless-2)
Homo sapiens (Human)
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83.3%; Score 35; DB 4;

Best Local Similarity 57.1%; Pred. No. 50;

Matches 4; Conservative 3; Mismatches (
685 AA.
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ne : 17.8384 secs
PRELIMINARY;
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216 CIPISSC 222

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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                             Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442248/47
                                                                                                                                                                                                                                                                                                    Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                               WO200152875-A1
                                                                                                                                                                                                                      26-SEP-2001
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                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              residues
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Aau62562 Propionib
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                                       2004, 09:37:49; Search time 22.9798 Seconds (without alignments) 86.068 Million cell updates/sec
                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                               Abg13170
Abb16042
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Abb96569
Aau18859
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Abg30203
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5.1.6
Compugen Ltd.
                                                                                                                                  of hits satisfying chosen parameters:
                                                                                                                     1586107 seqs, 282547505 residues
GenCore version (c) 1993 - 2004
                         OM protein - protein search, using sw model
                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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ABMS9081
ABB13100
ABB16042
AAU64239
ABG30203
ABG30203
AABG30203
AAM96565
AAM96565
AAM96565
AAM94953
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AAU99293
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geneseqp2000s:*
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geneseqp2003as:*
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seq length: 200000000
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      Copyright
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Match Length
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26	27	28	59	30	31	32	33	2.4	* 1	35	36	3.7	. 0	0 1	39	40	41		7	43	44	• •	4. T

## ALIGNMENTS

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphanglogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. Location/Qualifiers
1. .7
/note= "This bond cyclises the peptide" Cendron A; Stacker S, AAU04530 standard; peptide; 7 AA VEGF based monocyclic peptide 8. (LUDW-) LUDWIG INST CANCER RES 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533 (first entry)

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

Example 1; SEQ ID NO 23757; 1069pp; English.

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one anino acid deleted prior to cyclisation are used to interfer with angiogenesis, consistent on a lymphangiogenesis in a mammal with a condition carried by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, heat or cold crama, substance-induced melovascularisation of the liver, excessive trauma, substance-induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability cor brain. The peptides are also used to modulate vascular permeability cor brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere cor brain and used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and district returns the peptides are condition and arthritis, psoriasis and district returns the combination with an anti-inflammatory agent, to treat and also used to return the peptides and physicial activity induced by vEGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes immunogenic protein #23458.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitcham JL, Wang St
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU62562 standard; protein; 50 AA.
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2001; 2001WO-US012865.
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L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating acne vulgaria.
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                                                                                                                                                                                                                                                                                                                                                                                                                       diabetic retinopathy
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CVPLTSC 7
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS59627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7 AA;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in polypeptides. The proteins and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by particulars. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyellitis), uveitis and endophthalmitis. The acnes is also involved in infections of bone, joints and chetral conserved in the inflammatory nervous system, however it is particularly involved in the inflammatory of presence or absence of P. acnes in a patient comprises contacting a presence or absence of P. acnes in a patient comprises contacting a correct and determining the amount of bound protein in the sample. The collypeptides may be used as antigens in the production of antibodies of specific for P. acnes proteins. These antibodies can be used to specific for P. acnes proteins. These antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by contacting in electronic format directly from WIPO at capence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Jones R, Carte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes predicted ORF-encoded polypeptide #23757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 23757; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 4
Pred. No. 38;
0; Mismatches
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Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABM59081 standard; protein; 50 AA.
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Zhang Y, Wang S, Jen S, Lodé
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                                                                                                                                                                                                        90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003033515-A1.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50 AA;
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30-MAR-2001; 2001WO-US008631.
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23-AUG-2000; 2000US-00649167.
                                                                                                                        Local Similarity 85.7
Les 6; Conservative
                                                                                                                                            22 CAPLTSC 28
                                                                                                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                    1 CVPLTSC 7
                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                            Sequence 50 AA;
                                                                                                                                                                                                                    WO200175067-A2.
                                                                                                                                                                                18-FEB-2002
                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                            11-OCT-2001.
                                                                                                                    Query Match
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of the constant of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective, antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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Pred. No. 53;
                                                                                                       Claim 20; SEQ ID NO 43529; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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24-FEB-2000;
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encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to diminuopenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a differention; fusion proteins comprising a polypeptide of the invention; antibodies against polypeptides of the invention; antibodies against polypeptides of the invention; antibodies against polypeptides of the invention; and an immune response specific for a P. acnes

Co polypucleotides, antibodies, fusion proteins. T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient. The P. acnes polypeptides, polypucleotides, antibodies, fusion proteins. T cell populations or antigen-presenting cells that express the qualitant. The P. acnes polypeptides, polypucleotides, antibodies, fusion proteins. T cell populations or antigen-presenting cells that express the collypeptides are useful for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polypucleotides, antibodies, fusion proteins. T cell populations or antigen-presenting cells that express the collypeptides are useful for diagnosing, preventing or treating acnes or primers for uncleic acid hybridisation. The vaccine composition is useful for the sequence represents a polypeptide predicted to be encoded by an ORF (open ceptements and protein protein of an immune response against P. acnes, or for treating and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open ceptements a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the frame with the vire invention, invention, invention, invention in
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food supplement; medical imaging; diagnostic; genetic disorder.
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2000US-0198123P. 2000US-0205515P. 2000US-0209467P. 2000US-0214886P.

19-MAY-2000; 07-JUN-2000; 28-JUN-2000; 30-JUN-2000;

New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

WPI; 2001-639362/73 N-PSDB; AAS77357.

2000US-0215135P

17-MAR-2000; 2000US-0190076P.

2000US-0186350P. 2000US-0189874P.

02-MAR-2000; 16-MAR-2000;

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01-SEP-2000; 2000US-022945P.
06-SEP-2000; 2000US-022945P.
06-SEP-2000; 2000US-023043PP.
06-SEP-2000; 2000US-0231243P.
06-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0231414P.
14-SEP-2000; 2000US-0231418P.
14-SEP-2000; 2000US-023149P.
14-SEP-2000; 2000US-023140P.
15-SEP-2000; 200US-023140P.
15-SEP-2000; 2000US-023140P.
15-SEP-2000; 2000US-023140P.
15-SEP-2000; 2000US-023140P.
15-SEP-2000; 2000US-023140P.
15-SEP-2000; 2000US-023140P.
15-SEP-2000; 2000US-023140P.
15-SEP
2000US-0216647P.
2000US-0216880P.
2000US-0217487P.
2000US-0217487P.
2000US-0218290P.
2000US-0220964P.
2000US-0220964P.
2000US-0220564P.
2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
2000US-0225214P.
2000US-0225218P.
2000US-0225268P.
2000US-022526P.
2000US-0225475P.
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2000US-0229287P.
2000US-0229343P.
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
12-AUG-2000;
22-AUG-2000;
22-AUG-2000;
30-AUG-2000;
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20-OCT-2000; 2000US-0241809P.
20-OCT-2000; 2000US-0241826P.
20-OCT-2000; 2000US-0244647P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 200US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000US-0256719P. 2000US-0251479P. 2000US-0251856P. 2000US-0251868P. 2000US-0251990P 2000US-0251869P 2000US-0251989P 2001US-0259678P 05-JAN-2001; 

Ruben SM (HUMA-) HUMAN GENOME SCI INC. Rosen CA, Barash SC,

WPI; 2001-541565/60. N-PSDB; ABA12368.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.

Claim 11; SEQ ID NO 4699; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,

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disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischeemias; (d) wound healing infectious diseases such as myocardial ischeemias; (d) wound healing infections diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                 immune
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breast, gastrointestinal tract, liver, lung, or urogenital,
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68;
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Pred. No.
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85.7%; Pred
0; 1
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28 CXPLTSC 34

RESULT 6

Propionibacterium acnes immunogenic protein #25135. AAU64239 standard; protein; 91 AA. (first entry) 27-FEB-2002 AAU64239; 

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes.

WO200181581-A2

01-NOV-2001

20-APR-2001; 2001WO-US012865.

21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P.

(CORI-) CORIXA CORP.

Bhatia A; Wang SS, Mitcham JL, Wang S; , Jen S, Carter D; maisonneuve J, Zhang Y, Skeiky YAW, Persing DH,

WPI; 2001-616774/71. N-PSDB; AAS59641 Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.

Example 1; SEQ ID NO 25434; 1069pp; English.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a cares. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. Praces is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention

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                                                                                       used as
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for
and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. across proteins. These antibodies can be used to downregulate expression and activity of P. across polypeptides and therefore treat P. across infections. The antibodies may also be used diagnostic agents for determining P. across presence, for example, by enzyme linked immunosorbent assay (ELISA) Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 1.4e+02;
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85.7%;
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Best Local Similarity
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Propionibacterium acnes predicted ORF-encoded polypeptide #25434. Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine. ABM60758 standard; protein; 91 AA. (first entry) 20-OCT-2003 ABM60758; 

Propionibacterium acnes. WO2003033515-A1.

11-OCT-2002; 2002WO-US032727. 24-APR-2003

15-OCT-2001; 2001US-00978825.

(CORI-) CORIXA CORP.

Maisonneuve JL; Jones R, Carter D; Skeiky YAW, Persing DH, Bhatia A, ng S, Jen S, Lodes MJ, Benson DR, Wang S, Jen S, Lode Vallieve-Douglass J; Mitcham JL, Zhang Y, Wa Barth B, Va

2003-381789/36. N-PSDB; ACF64570

polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. New Propionibacterium acnes polypeptides and polynucleotides encoding

Example 1; SEQ ID NO 25434; 1481pp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABMS624-ABM64536) and to additionally encompasses expression vectors and host cells comprising additionally encompasses expression vectors and host cells comprising a polypucleotide of the invention; antibodies against polypeptides of the invention; an invention; antibodies against polypeptides of the invention; an invention a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a

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patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynuclectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polympeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynuclectides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present cand the kit is useful for performing a diagnostic assay. The present canding frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oilgomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 6; I
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #30194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG30203 standard; protein; 4561 AA
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23-AUG-2000; 2000US-00649167.
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85.7%;
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                                                                                                                                                                                                                                                                                                                 Sequence 91 AA;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders
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supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG0030377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #21055.
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                                                                                                                                                                                                                                                     Sequence 4561 AA;
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2000US-0246611P
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30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
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08-NOV-2000; 2
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08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 3
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13-OCT-2000;
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involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                        Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy.
                                                                                                                                                               Gaps
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0
                                                                                                                                        85.7%; Score 36; DB 4; Length 9222; 71.4%; Pred. No. 8.2e+03;
                                                                                                                                                                                                                                                                                                                  Human reproductive system related antigen SEQ ID NO: 5223.
                                                                                                                                                              0; Indels
                                                                                                                                                            2; Mismatches
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24-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0180636P.
02-MAR-2000; 2000US-0189364P.
16-MAR-2000; 2000US-0189374P.
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14-AUG-2000; 2000US-0225266P.
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2000US-0225758P.
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                                                                                                                           Query Match
Best Local Similarity 71.4%,
Thes 5; Conservative
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                                                                                                                                                                                                   3655 CVPISSC 3661
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                                                                                                                   Sequence 9222 AA;
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reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic.
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14-SEP-2000;
21-SEP-2000;
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14-AUG-2000; 2
14-AUG-2000; 2
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83.3%; Score 35; DB 4; Length 61;

Best Local Similarity 85.7%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 1; Indels
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17-NOV-2000; 2000US-0259360P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250310P.
05-DEC-2000; 2000US-025193P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-02519F.
06-DEC-2000; 2000US-025186F.
08-DEC-2000; 2000US-0251866P.
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2000US-0251990P.
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N-PSDB; AAL02535.
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01-NOV - 2000; 2000US - 024617P.
08-NOV - 2000; 2000US - 0246475P.
08-NOV - 2000; 2000US - 0246475P.
08-NOV - 2000; 2000US - 0246476P.
08-NOV - 2000; 2000US - 0246523P.
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08-NOV - 2000; 2000US - 0246528P.
08-NOV - 2000; 2000US - 0246532P.
08-NOV - 2000; 2000US - 0246532P.
08-NOV - 2000; 2000US - 0246532P.
08-NOV - 2000; 2000US - 024651P.
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17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249265P.
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13-OCT-2000; 2000US-0239937P
20-OCT-2000; 2000US-0240960P
20-OCT-2000; 2000US-0241221P
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02-OCT-2000; 2
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The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and agastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a protein of the
                                                                                                                                            Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antianaemic; dermatological; immunosupressive; antinflammatory; antiantarthritic; antirheumatic; virucide; hepatotropic; nephrotropic; osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasia; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; autoimmune disorder; urinary system; system; lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; endocrine disorder; inflammatory disorder; liver disorder; wound healing; food preservative.
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85.7%; Pred. No. 1.4e+02;
ive 0; Mismatches 1; Indels
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                                                                                                                                                                                            Claim 11; SEQ ID NO 1953; 766pp; English.
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                                                                                  Ruben SM;
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24 -FEB-2000; 2000US-018664P.
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11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                              (HUMA-) HUMAN GENOME SCI INC
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Matches 6; Conservative
                                                                                Barash SC,
                                                                                                               WPI; 2001-483232/52.
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11-JUL-2000; 2000US-021748PP.
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14-SEP-2000; 200US-033139P.
14-SEP-2000
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2000US-0241221P.
2000US-0241785P.
2000US-0241786P.
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20-OCT-2000; 2000US-0241787P.
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01-NOV-2000; 2000US-024647P.
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM

WPI; 2001-476223/51. N-PSDB; AAS30300.

Novel isolated prostate gland related polypeptide useful for diagnosis and treatment of disorders of prostate such as prostatodystonia, prostatosis, prostatitis, benign prostatic hypertrophy and malacoplakia.

Claim 1; SEQ ID NO 158; 512pp; English.

The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prognosis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, prostatodystonia, prostaticis, granulomatous prostatitis, malacoplakia, benign prostatic

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2000US-0225759P
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2000US-0221882P
2000US-0227182P
2000US-0227168P
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2000US-0246528P
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13-OCT-2000;
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             hypertrophy or hyperplasia, and prostate neoplastic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas. [1], (II) and antibody to (II) are useful for diagnosing and treating reproductive system disorders (Paget's disease), autoimmune disorders (system disorders) returnitis), thood-related disorders (sickle cell anaemia), hyperproliferative disorders, urinary system disorders (arrhythmias), respiratory (glomerulonephritis), cardiovascular disorders (arrhythmias), respiratory cardiovascular disorders (arrhythmias), respiratory candorance, musculoskeletal system disorders (arrhythmias), and fisease), cendocrine disorders (Alzhemer's disease and Parkinson's disease), cendocrine disorders (Alzhemer's disorders (biliary liver cirrhosis), pancreatic and gall bladder disorders (biliary liver cirrhosis), pancreatic and gall bladder disorders, diseases at the cellular level, and wound healing and epithelial cell proliferation. (I) or (II) is useful to prevent skin aging, for preventing hair loss, to maintain
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83.3%; Score 35; DB 4; Length 65;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels
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24-FRB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0184674P.
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28-JUN-2000; 2000US-0214886P.
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CLPLSSC 47
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Best Local Similarity
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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                                 08-NOV-2000;
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                                                                                                                                                                                         7-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
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polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by a cnes. The disorders include SAPHO syndrowitis, acre, or practices and osteomyelitish), uveitis and endophthalmitis. The cuests is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory resence or absence of P. acres in a partient comprises contacting a presence or absence of P. acres in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies of specific for P. acres proteins. These antibodies can be used to downregulate expression and activity of P. acres polypeptides and chermining P. acres presence. For example, by charged immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was the contact of the printed specification, but was contactive and activity from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                          SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                      Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 4; Length 80;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
             Propionibacterium acnes immunogenic protein #9908.
                                                                                                                                                                                                                                                                                                                                                                                                    Mitcham JL, Wang S. Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 10207; 1069pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM45531 standard; protein; 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.3%;
                                                                                                                                                                                                                                                                                        21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                       20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                                                                        Persing DH, M: J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85...
6; Conservative
                                                                                                                                             Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-616774/71.
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                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                           L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS59543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80 AA;
                                                                                                                                                                                 WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YAW,
                                                                                                                                                                                                                      01-NOV-2001.
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The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a collypeptide of the invention; antibodies against polypeptides of the invention; tuston proteins comprising a polypeptide of the invention; and an isolated T cell population comprising T cells prepared to polypeptide of the invention; and this method; a vaccine composition (comprising P acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations, or contigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a proteins. T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes or primers for nucleic acid hybridisation. The vaccine composition is useful for the studies can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for performing a diagnostic assay. The present can the kit is useful for performing a diagnostic assay. The present can apolypeptide predicted to be encoded by an ORF (open cading frame) contained within the P. acnes polymolectides of the printed specification, but was obtained in electronic format directly from mive the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Maisonneuve JL;
Jones R, Carter D;
                      Propionibacterium acnes predicted ORF-encoded polypeptide #10207.
                                                                      Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 10207; 1481pp; English
                                                                                                                                                                                                                                                                                          11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                       15-OCT-2001; 2001US-00978825.
                                                                                                                                             Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-381789/36.
N-PSDB; ACF64472.
                                                                                                                                                                                             WO2003033515-A1
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Query Match

Query Match

Best Local Similarity 85.7%; Pred. No. 1.8e+02;

Matches 6; Conservative 0; Mismatches 1; Indels

Qy 1 CVPLTSC 7

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Gaps

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> Search completed: September 5, 2004, 09:55:17 Job time: 25.9798 secs

37 CDPLTSC 43

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100.0%; Score 42; DB 9; Length 7; llarity 100.0%; Pred. No. 1.2e+06; Conservative 0; Mismatches 0; Indels
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; Sequence 248060, Application US/10424599
; Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
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CVPLTSC
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  SEQ ID NO 11
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Sequence 3611, Ap
Sequence 5, Appli
Sequence 1832, Ap
Sequence 48, Appl
Sequence 1835, Ap
Sequence 1835, Ap
Sequence 58, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Appl
Sequence 248060,
Sequence 199668,
Sequence 118478,
                                                                                                                                                                    September 5, 2004, 10:00:15; Search time 19.6566 Seconds (without alignments) 112.199 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_Pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_Pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NBW_PUB_Pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NBW_PUB_Pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NBW_PUB_Pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-761-636A-11
US-10-424-599-248060
US-10-424-599-199668
US-10-437-963-118478
US-09-764-891-5223
US-09-764-891-5223
US-09-764-891-5223
US-10-99-764-891-3611
US-09-833-245-1835
US-10-991-254-48
US-10-99-833-245-1835
US-09-833-245-1835
US-10-1016-248-58
US-10-110-018-16
US-10-110-018-16
US-10-110-018-16
US-10-110-018-16
US-10-110-018-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1298764 segs, 315065143 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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42
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Match Length DB
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253
753
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83.3
83.3
                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
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Sequence 3546, Applisequence 1244, Applisequence 1243, Applisequence 1246, Applisequence 906, Applisequence 906, Applisequence 465, Applisequence 2, Applisequence 1116, Applisequence 1156, Applisequence 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Appl
Sequence 8827, Ap
Sequence 8828, Ap
Sequence 104490,
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Sequence 33904, A
Sequence 219, App
                                                                        Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT FILING DATE: 2001-01-18
PRIOR PELICATION NUMBER: US 60/176, 293
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR PLING DATE: 2000-01-18
PRIOR PLING DATE: 2000-01-18
PRIOR PLING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
      Sequence
Sequence
Sequence
4 US-10-120-018-12
2 US-10-263-929-116
2 US-10-108-9
5 US-10-108-9
6 US-10-108-260A-3546
6 US-10-112-944-424
2 US-10-112-944-424
4 US-10-029-386-29056
2 US-10-112-944-465
2 US-10-112-944-465
2 US-10-112-944-906
4 US-10-112-944-906
5 US-10-112-944-906
5 US-10-112-944-906
6 US-10-10-29-189382
7 US-10-28-217-1116
7 US-10-28-218-1158-116
7 US-10-29-1189382
7 US-10-29-1189382
7 US-10-29-1189382
7 US-10-29-118-9-18802
7 US-10-424-599-1189382
7 US-10-424-599-1189382
7 US-10-424-599-1189382
7 US-10-437-963-104490
7 US-10-313-97-8828
7 US-10-335-977-8828
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7 US-10-335-977-8828
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sequence 11, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
      646
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721
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Gaps

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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF INVENTION: 91-21 (53221) B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NOS: 204966 SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (60)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-5223
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5223, Application US/09764891
; Dublication No. US20030077808A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBNCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3111
LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.3%; Score 35; DB 10; Length 61; 85.7%; Pred. No. 81;
                                                                                                                                                                                                                                                                    Length 75;
                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                            , OTHER INFORMATION: Clone ID: PAT_MRT4530_21786C.1.pep
US-10-437-963-118478
                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                   Score 36; DB 1
Pred. No. 66;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3611, Application US/09764891; Publication No. US20030077808A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    85.7%;
71.4%;
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Best Local Similarity 71.4
Matches 5, Conservative
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                                                                                                                                                       TYPE: PRT
ORGANISM: Oryza sativa
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ORGANISM: Homo sapiens
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Matches 6; Conserv
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LOCATION: (58)
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US-09-764-891-3611
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APPLICANT: Rovalic David K
APPLICANT: Choury thus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 248060
LENGTH: 118
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Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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US-10-424-599-248060
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US-10-424-599-199668
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Sequence 118478, Application US/10437963

Publication No. US2040123343A1

GRNERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei
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Barbazuk, Brad
Li, Ping
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85.7%;
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Best Local Similarity 85.7°
----- 6; Conservative
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Best Local Similarity 85...
6. Conservative
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ORGANISM: Glycine max
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FILE REFERENCE: PTZ06C1
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                            %Sequence 5, Application US/10120018
; Sequence 5, Application US/10120018
; Publication No. US20030194708A1
; GENERAL INFORMATION:
; APPLICANT: Binnerts et al
; TITLE OF INVENTION: Human Homolog of Crossveinless Materials and Methods
; FILE REFERENCE: 28110/37995
; CURRENT PPLICANTION NUMBER: US/10/120,018
; CURRENT FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.0
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                                                                           Score 35; DB 10; Length 65;
Pred. No. 86;
2; Mismatches 0; Indels
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Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REPERENCE: PF946CT
CURRENT APPLICATION NUMBER: 05/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR PELING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR PELING DATE: 2000-12-21
PRIOR PELING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR PELING DATE: 2000-12-21
SPIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PALENT UNIVER: 2000-04-25
LENGTH: 270
                                                                             83.3%;
illarity 71.4%;
Conservative
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ORGANISM: Homo sapiens
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-3611
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CRGANISM: Homo sapiens
US-10-120-018-5
                                                          Query Match
Best Local Similarity
5; Conserv
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50 CIPISSC 56
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Best Local Similarity
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LENGTH: 19
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| DCOMITON: (0268) | DCOMITON: (0269) | DCCORRESTATION: (0269)
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NUMBER: 60/241, 809 2000-10-20 NUMBER: 60/249, 299 2000-11-17 NUMBER: 60/236, 327 2000-09-29 NUMBER: 60/244, 617 2000-110-10 NUMBER: 60/244, 617 2000-11-01 NUMBER: 60/225, 268 2000-08-14 NUMBER: 60/225, 268 2000-08-14	NUMBER: 60/251, 2000-12-08 (2000-12-08) (2000-11-08) (2000-11-08) (2000-11-08) (2000-11-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-08) (2000-11-12-12-08) (2000-11-12-12-08) (2000-11-12-12-08) (2000-11-12-12-08) (2000-11-12-12-08) (2000-11-12-12-12-08) (2000-11-12-12-12-12-12-08) (2000-11-12-12-12-12-12-12-12-12-12-12-12-12-	SER 00- 00- 00- BER 00-
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R FILING DATE: 2000-09-06
R APPLICATION NUMBER: 60/215,135
R FILING PATE: 2005-06-30
R APPLICATION NUMBER: 60/225,266
R FILING DATE: 2000-08-14
R APPLICATION NUMBER: 60/249,218 TAPPLICATION WIMBER: 60/232,080

R FILING DATE: 2000-09-08

R FILING DATE: 2000-09-08

R FILING DATE: 2000-09-08

R APPLICATION NUMBER: 60/231,244

R FILING DATE: 2000-09-08

R FILING DATE: 2000-09-08

R FILING DATE: 2000-09-08

R FILING DATE: 2000-09-09

R FILING DATE: 2000-09-14

R APPLICATION NUMBER: 60/233,064 R FILING DATE: 2000-11-17
R FILING DATE: 2000-11-17
R FILING DATE: 2000-09-14
R PILING DATE: 2000-09-08
R FILING DATE: 2000-09-08
R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/231,242
R FILING DATE: 2000-09-08 R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/241,826
R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/241,786
R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/241,221 APPLICATION NUMBER: 60/235,836 FILING DATE: 2000-09-27 APPLICATION NUMBER: 60/230,438 FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,208
FILING DATE: 2000-11-17 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,212 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,215 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,264 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,245 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,244 FILING DATE: 2000-09-14 APPLICATION NUMBER: 60/232,397 FILING DATE: 2000-09-14 FILING DATE: 2000-09-14 APPLICATION NUMBER: 60/232,399 FILING DATE: 2000-09-14 APPLICATION NUMBER: 60/246,475 FILING DATE: 2000-11-08 APPLICATION NUMBER: 60/231,243 APPLICATION NUMBER: 60/249,213 APPLICATION NUMBER: 60/249,207 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,217 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,211 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,214 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,297 APPLICATION NUMBER: 60/232,401 FILING DATE: 2000-09-14 APPLICATION NUMBER: 60/241,808 FILING DATE: 2000-10-20 FILING DATE: PRIOR PRIOR

Query Match 83.3%; Score 35; DB 14; Length 270; Best Local Similarity 57.1%; Pred. No. 3.16+02; Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps

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Publication No. US20040010134A1
GENERAL INFORMATION:
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
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Sequence 58, Application US/10016248
Publication No. US20040033491A1
GENERAL INFORMATION:
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Matches 4; Conservative
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336 CIPISSC 342
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: misc feature
LOCATION: (113)
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CIPISSC 167
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161 CIPISSC 167
                                   1 CVPLTSC 7
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; Sequence 1835, Application US/09833245

RESULT 11 US-09-833-245-1835

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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-218
CURRENT APPLICATION NUMBER: US/10/016,248
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/833,24

PRIOR APPLICATION NUMBER: 60/229, 358

PRIOR FILING DATE: 2000-04-12

PRIOR PLING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/256, 931

PRIOR FILING DATE: 2000-12-21

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: PATENTIN VEY: 2.1

SEQ ID NO 1835

LENGTH: 445
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PRIOR APPLICATION NUMBER: 60/254,329
PRIOR APPLICATION NUMBER: 60/254,329
PRIOR PLING DATE: 2000-12-08
PRIOR PELING DATE: 2001-05-15
PRIOR PELING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-00-31
PRIOR FILING DATE: 2001-10-11
PRIOR FILING DATE: 2001-10-11
PRIOR FILING DATE: 2001-00-31
PRIOR FILING DATE: 2001-00-31
PRIOR FILING DATE: 2001-00-31
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
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Search completed: September 5, 2004, 10:29:21 Job time: 20.6566 secs
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US-10-451-417-4
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US-10-120-018-16
i Sequence 16, Application US/10120018
i Deducation No. US20030194708A1
i GENERAL INFORMATION:
GENERAL INFORMATION:
I TITLE OF INVENTION: Human Homolog of Crossveinless Materials and Methods
FILE REFERENCE: 28110/37995
CURRENT APPLICATION NUMBER: US/10/120,018
CURRENT FILING DATE: 2002-04-10
NUMBER OF SEQ 1D NOS: 17
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/10120018
Sequence 17, Application US/10120018
Publication No. US20030194708A1
GENERAL INFORMATION:
APPLICANT: Binnerts et al
TITLE OF INVENTION: Human Homolog of Crossveinless Materials and Methods
FILE REFERENCE: 28110/37995
CURRENT APPLICATION NUMBER: US/10/120,018
CURRENT FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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                                                                                                     Query Match 83.3%; Score 35; DB 12; Length 462; Best Local Similarity 71.4%; Pred. No. 5.1e+02; Matches 5; Conservative 2; Mismatches 0; Indels
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Pred. No. 5.1e+02;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (312)..(312)
OTHER INFORMATION: wherein "X" is unknown or other
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OTHER INFORMATION: wherein "X" is unknown or other
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NAME/KEY: MISC FEATURE
LOCATION: (307)...(307)
OTHER INFORMATION: wherein "X" is unknown or
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Best Local Similarity 71.4%;
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NAME/KEY: MISC FEATURE
                 ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-016-248-58
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; ORGANISM: Mus musculus
US-10-120-018-16
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ORGANISM: Homo sapiens
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113 CVPVSSC 119
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113 CVPVSSC 119
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LENGTH: 462
LENGTH: 462
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                                                                                                Length 464;
                                                                                             83.3%; Score 35; DB 14; Length 46
57.1%; Pred. No. 5.1e+02;
ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10451417

Sequence 4, Application US/10451417

Publication No. US20040110921A1

GENERAL INFORMATION:
APPLICANT: ORITA, Satoshi et al
TILB OF INVENTION: A NOVEL POLYPEPTIDE AND ITS DNA
FILE REFERENCE: 0032-0276P

CURRENT APPLICATION NUMBER: US/10/451,417

CURRENT FILING DATE: 2000-06-23

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 627
) NAME/KEY: MISC FEATURE
) LOCATION: (462)...(462)
) OTHER INFORMATION: wherein "X" is unknown or other
US-10-120-018-17
                                                                             Query Match
Best Local Similarity 57.1.
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ORGANISM: Homo sapiens
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355 CIPISSC 361
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Best Local Similarity
Matches 4; Conserva
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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507 CLPMTSC 513
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Matches 5; Conser
      US-09-134-000C-6380
TYPE: PRT
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33012, A
29595, A
27, Appl
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Sequence 29358, A
Sequence 2, Appli
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                                                         09:55:30 ; Search time 6.2222 Seconds (without alignments) 58.079 Million cell updates/sec
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/cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-134-000C-6380

US-09-252-991A-29358

US-08-718-388-7

US-08-718-388-9

US-08-969-106-11

US-09-38-125-11

US-09-904-615-92

US-09-904-615-92

US-09-252-991A-22994

US-09-252-991A-22994

US-09-252-991A-22994

US-09-252-991A-22994

US-09-252-991A-22994

US-09-252-991A-22995

US-09-252-991A-22996

US-09-252-991A-22995

US-09-252-991A-22995

US-09-252-991A-22995

US-09-252-991A-2295

US-08-31-565A-27

US-09-267-439-121

US-09-267-439-121

US-09-267-439-121

US-09-267-439-121

US-09-267-439-121

US-09-267-439-121

US-09-134-000C-6451

US-09-134-000C-6451

US-09-226-710-21

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Maximum Match 100%
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                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                           5, 2004,
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Match Length
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28 31 73.8 12 3 US-08-742-243-35 Sequence 35, Appl 30 173.8 12 3 US-08-742-243-36 Sequence 36, Appl 31 73.8 12 3 US-08-742-243-37 Sequence 37, Appl 31 73.8 12 3 US-08-742-243-38 Sequence 37, Appl 32 31 73.8 17 3 US-08-07-992B-23 Sequence 23, Appl 34 31 73.8 45 4 US-09-716-129-94 Sequence 24, Appl 35 31 73.8 100 3 US-08-07-794-31 Sequence 12, Appl 36 31 73.8 110 4 US-09-574-708-11 Sequence 11, Appl 37 31 73.8 110 4 US-09-574-708-11 Sequence 11, Appl 40 31 73.8 110 4 US-09-392-931-10 Sequence 11, Appl 40 31 73.8 110 4 US-09-392-931-10 Sequence 11, Appl 41 31 73.8 120 6 5194596-9 Patent No. 5194596 Patent No. 5194596
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### AL I GNMENTS

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RESULT 1
US-09-134-000C-6380

Sequence 6380, Application US/09134000C

Sequence 6380, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:
TITLE OF INVENTION:
THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/055,778

FRIOR FILING DATE: 1997-08-13

SEQ ID NO 6380

LENGTH: 616

TYPE: PRIOR
TYPE: PRIOR
TITLE OF INVENTION:
THERAPEUTICS

OVER ON THE OF TITLE OF THE OF
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RESULT 2

US-09-252-991A-29358

US-09-252-991A-29358

Satent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION

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US-08-718-388-9; Sequence 9, Application US/08718388; Patent No. 6271362
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CLASSIFTCATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WIREHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.0%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-388-7
CORRESPONDENCE ADDRESS:
             ADDRESSEE: BIRCH, S
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1183 CLPLASC 1189
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APPLICANT: Hardy, Daniel M.
APPLICANT: Garbers, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
TITLE OF INVENTION: Sperm
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.0%; Score 34; DB 2; Length 2476; 71.4%; Pred. No. 9.7e+02; Live 1; Mismatches 1; Indels
                                     81.0%; Score 34; DB 4; Length 394; 71.4%; Pred. No. 1.7e+02; ive 1; Mismatches 1; Indels
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| Patent NO. 6271362
| GENERAL INFORMATION:
| APPLICANT: MORIKAWA, MINORU
| APPLICANT: HARADA, NAOKI
| TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING
| TITLE OF INVENTION: PROTEIN
| NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUNTRY: HOUSELOUS
STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: UTSD:418\KIT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-789-2679
                                                                                                                                                                                                                                                       Sequence 2, Application US/08276967 Patent No. 5851817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino acids
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Best Local Similarity 71.*.
                                         Ouery Match
Best Local Similarity 71.4
Matches 5; Conservative
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     US-09-252-991A-29358
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US-08-718-388-7
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US-08-276-967-2
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Pred. No. 1e+03;
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APPLICANT: MORIKAWA, MINORU
APPLICANT: HARADA, NACHI
APPLICANT: HARADA, NACHI
TILE OF INVENTION: GENE ENCODING 19G FC REGION-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
                                                                                                            CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TREE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATENIN PC compatible
COMPUTER: APPELICATION DATA:
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
E: BIRCH, STEWART, KOLASCH AND BIRCH
PO BOX 747
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FILING DATE:
CLASSIFTCATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: WINEPY LAY, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0230-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8000
TELEPAX: (703) 205-8000
TELEPAX: (703) 205-8050
SEQUENCE CHARACTERISTICS:
TENDRAMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TENDRAMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TENDRAMATION ACCURATE ACCU
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-338-125-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036
COMPUTER READBLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13.NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leelle
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
TELECHOME: 212-790-9090
TELEFOND INFORMATION:
TELEFOND SOFT INFORMATION:
TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yang, M.
APPLICANT: Yang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Schulz, V.
ITILE OF INVENTION: CDK2 INTERACTIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08969106
Patent No. 5986055
GENERAL INFORMATION:
                        SEQUENCE CHARACTERISTICS:

LENGTH: 5405 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-718-388-9
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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; MOLECULE TYPE: protein
US-08-969-106-11
                                                                                                                                                                                                                                       1183 CLPLASC 1189
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US-08-969-106-11
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Sequence 11, Application US/09338125 Patent No. 6521412

US-09-338-125-11

RESULT 7

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Gaps
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| Sequence 2, Application US/08875972
| Patent No. 5985564
| GENERAL INFORMATION:
| APPLICANT: HUNDINGTON POLTER and Jinhue Li
| TITLE OF INVENTION: ASSAY FOR IDENTIFYING GENES
| TITLE OF INVENTION: CHROMOSOME NON-DISJUNCTION
| NUMBER OF SEQUENCES: 29
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C. STREET: Two Militia Drive
| CITY: Lexington | STATE: Massachusetts
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.6%; Score 33; DB 4; Length 280; 71.4%; Pred. No. 1.9e+02; ive 0; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Yang, M.
APPLICANT: Nandabalan, K.
APPLICANT: Schulz, V.
TITLE OF INVENTION: CDK2 INTERACTIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FRSESEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,125
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PAROS FICTORATION:
APPLICATION DATA:
APPLICATION NUMBER: US/08/969,106
FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 280 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.4
Matches 5, Conservative
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                     New York
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Query Match 76.2
Best Local Similarity 71.4
Matches 5, Conservative
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90 CMPPTSC 96
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                                                                                                                                                                                              ; ORGANISM: Pseudo
US-09-252-991A-22994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM:
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Pred. No. 2.4e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 92, Application US/09904615; Patent No. 6566325; General Reperburian No. 49 Human Secreted Proteins; TILLE OF INVENTION: 49 Human Secreted Proteins; CURRENT APPLICATION NUMBER: US/09/904,615; CURRENT FILING DATE: 2001-07-16; PRIOR APPLICATION NUMBER: 60/097,917; PRIOR FILING DATE: 1998-08-25; PRIOR PILING DATE: 1998-08-25; PRIOR PILING DATE: 1998-08-31; NUMBER: OF SEQ ID NOS: 170; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (68)
OTHER INFORMATION: Xaa equals stop translation
        RESULT 10
US-09-252-991A-22994
; Sequence 22994, Application US/09252991A
; Patent NO 655/795
; GENERAL INPORMATION:
; APPLICANT: Marc J. Rubenfield et al.
APPLICATION NUMBER: US/08/875,972
                                                                                                                                                                                                                                                                                                                            78.6%;
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Best Local Similarity 71.4
Matches 5; Conservative
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Matches 5, Conservative
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38 IPLTSC 43
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LOCATION: (68)
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| TITLE OF INVARION, ARROCINGAR FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVARION, ARROCINGAR FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVARION ARROCINGAR FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVARION ARROCINGAR FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVARION ARROCINGAR FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF APPLICATION NUMBER: US 60/044.300
| PRIOR FILLING DATE: 1399-0-120 |
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TYPE: amino acid
STRANDEDNESS: Unl
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296 IPLTSC 301
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Best Local Similarity
Matches 5; Conserv
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NEW YORK
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US-08-231-565A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: 1
STATE:
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THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
                                                                                    Score 32; DB 4; Length 382;
Pred. No. 3.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 2; Length 661;
Pred. No. 6.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 Sequence 27, Application US/08417174
Patent No. 5844075
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
TILLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STATE: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-ARP-1995
FRIOR APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION NUMBER: 37,341
RECISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US
TELECOMMUNICATION INCRAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-417-174-121
; Sequence 121, Application US/08417174
; LENGTH: 382
; TYPE: PR
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29595
                                                                              Query Match 76.2%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: Unknown
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Protein
                                                                                                                                                                          1 CVPLTSC 7
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296 IPLTSC 301
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                   US-08-417-174-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-417-174-27
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                                                                    MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
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THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
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Pred. No. 6.1e+02;
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                                                                                                                                                                                                                                                                                                               COMPUTER REALDSLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION NUMBER: 37,341
REFERENCE CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REGISTRATION NUMBER: 37,341
REGISTRATION NUMBER: 37,341
REGISTRATION NUMBER: 37,341
RELECOMMUNICATION INFORMATION:
TELEPONE: (212) 759-4800
TELEPAN: A31707
TELEPAN: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: METHODS
ITTLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS A
TITLE OF INVENTION: METHODS
                                                                                                                                  NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/08231565A
Patent No. 5874560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.2%;
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MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC COMPATIBLE
COMPUTER: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565A
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPH:
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124
TELECOMUNICATION: 1878-4800
TELECAN: (212) 758-4800
TELECAN: (212) 758-480
TELECAN: (212) 758-480
TELECAN: (212) 758-480
TELECAN: (212) 758-864
INPORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 661
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Protein
US-08-231-5658-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|||||
296 IPLTSC 301
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Search completed: September 5, 2004, 10:21:59 Job time : 6.22222 secs

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

Run on:

September 5, 2004, 09:47:29; Search time 4.60606 Seconds (without alignments) 125.302 Million cell updates/sec

US-09-761-636A-12 38 1 CVPLTC 6 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES	Description	74	21 hypothetical prot	54 pregnancy-associa	4	33 adenosine recento	26 endothelin	0 transposase	0 probable eth	8	1-phosphatic	2	33 hypothetical	64 probable per	59 two-compo	Cottonlasmic d		apolipoprotejn H				63 qlycoprotein GP330		qp330 proteir	beta-defensin-5 -	06 hypotherical	hypothetical		019 hypothetical prote	. (
0)	ID	T256	T276;	8654	T2091	I489	A541	AC239	T0805	A3449	A5397	S1298;	T264	C813	B826	T405	B43652	NBBO	A35281	T406	AD1930	A30363	JC5598	T427	E454	T296	T2706	C693	0	1
	DB	1 2	7	7	7	7	7	7	7	7	н	7	7	7	~	~	~	Н	~	~	~	7	7	~	7	N	~	7	7	c
	ouery Match Length	817	293	1627	367	332	415	467	637	650	1236	108	137	156	252	301	314	345	398	425	518	972	1034	4660	40	133	224	326	414	,
æ	Query Match	100.0	97.4	92.1	89.5	86.8	86.8	86.8	86.8	86.8	86.8	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	84.2	81.6	81.6	81.6	81.6	81.6	
	Score		37	35	34	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	31	31	31	31	31	2.1
	Result No.		7	m	4	Ŋ	9	7	œ	6		11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	90

mannose-1-phosphat hypothetical prote	RES4-25 protein	VLDL receptor prec	hypothetical prote	P-dlycoprotein - S	rough deal protein	hypothetical prote	beta-defensin-7 -	beta-defensin-9 -	beta-defensin-3 -	beta-defensin-6 -	airway epithelial	lingual antimicrob
AC3622 T24121	JE0188	JC4858	T26644 T29027	T30821	T13166	T00867	G45495	I45495	C45495	F45495	A47438	A56128
2 2	9.0	11	0 0	1 (1)	~	~	~	~	N	~	7	7
471 588	718	869	1042	1451	2098	2946	40	40	42	42	64	64
81.6 81.6	81.6	81.6	81.6	81.6	81.6	81.6	78.9	78.9	78.9	78.9	78.9	78.9
31	31	31	33	31	31	31	30	30	30	30	30	30
30 31	3.2	34	35	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

		Caenorh
		- 1
		F08D12.6
		protein
RESULT 1	T25674	hypothetical

abditis elegans

C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999 C;Accession: T25674

Rile, T.; Waterston, R. submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid F08D12. A;Reference number: Z20068

A;Accession: T25674
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DMA
A;Residues: 1-817 <LET>
A;Cross-references: EMBL:U80840; PIDN:AAB37929.1; GSPDB:GN00020; CESP:F08D12.6
A;Experimental source: strain Bristol N2; clone F08D12
C;Genetics:

A;Gene: CESP:F08D12.6 A;Map position: 2 A;Introns: 27/2; 329/3; 407/1; 477/3; 538/3; 622/2

Gaps 0; Query Match 100.0%; Score 38; DB 2; Length 817; Best Local Similarity 100.0%; Pred. No. 18; Matches 6; Conservative 0; Mismatches 0; Indels

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ò Dp RESULT 2

hypothetical protein ZC504.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dect. 15-0ct-1999 #sequence\_revision 15-0ct-1999 #text\_change 18-Feb-2000
C;Accession: T27621
R;Kershaw, J.
R;

A;Gene: CESP:ZC504.5 A;Map position: X A;Introns: 40/3; 140/3; 173/3; 255/3

97.4%; Score 37; DB 2; Length 293; 83.3%; Pred. No. 12; Query Match Best Local Similarity .

Gaps

Matches

g ð

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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C;Accession: 14993
R;Marquardt, D.L.; Walker, L.L.; Heinemann, S.
J. Immunol. 152, 4508-4515, 1994
A;Title: Cloning of Two Adenosine Receptor Subtypes From Mouse Bone Marrow-Derived Mast A;Title: Cloning of Two Adenosine Receptor PwID:8157966
A;Accession: 148933
A;Accession: 148933
A;Accession: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-33 cRES
A;Cross-references: EMBL:U05673; NID:9498337; PIDN:AAA19001.1; PID:9498338
C;Superfamily: adenosine receptor A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-Unl-1995 #sequence_revision 07-Unl-1995 #text_change 16-Uul-1999
C;Accession. 454126
R;Kumar, C.; Mwangi, V.; Nuthulaganti, P.; Wu, H.L.; Pullen, M.; Brun, K.; Aiyar, H.; M.; Biol. Chem. 269, 13414-13420, 1994
A;Title: Cloning and characterization of a novel endothelin receptor from Xenopus heart A;Reference number: A54126; MUID:94230448; PMID:817572
A;Accession. A54126
A;Acce
                                Ajaccession: T20914
Ajstatus: preliminary; translated from GB/EMBL/DDBJ
Ajmolecule type: DML>
Ajmolecule type: MLL>
Ajcross-references: EMBL: Z92782; PIDN: CAB07186.1; GSPDB: GN00023; CESP: F14F8.5
Ajcross-references: clone F14F8
Ajcross-references: Ajcross-references: Ajcross-references: Ajcross-references: Clone F14F8
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Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB
Pred. No. 50;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 23/3; 97/2; 145/2; 301/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - monse
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Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.8%;
83.3%;
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Best Local Similarity 83.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenosine receptor subtype
A; Reference number: Z19346
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Best Local Similarity
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92 CIPVTC 97
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A; Readdues: 77-1627 <KRS>

A; Readdues: 77-1627 <KRS>

A; Cross-references: GB:X66280; NID:G394649; PIDN:CAA48341.1; PID:G394650

B; Oxvig, C.; Sand, O.; Kristensen, T.; Gleich, G.J.; Sottrup-Jensen, L.

B; Disol. Chem. 268, 12243-12246, 1993

A; Title: Circulating human pregnancy-associated plasma protein-A is disulfide-bridged to

A; Reference number: 138097; MUID:93286045; PMID:7685339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: EMBL:U28727
A;Note: the authors translated the codon CGA for residue 101 as Thr
R;Kristensen, T.; Oxvig, C.; Sand, O.; Moller, N.P.H.; Sottrup-Jensen, L.
Biochemistry 33, 1592-1598, 1994
A;Title: Amino acid sequence of human pregnancy-associated plasma protein-A derived from
A;Reference number: A54220; MUID:94146014; PMID:7508748
                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 22-Nov-1996 #sequence revision 22-Nov-1996 #text_change 05-Nov-1999
C;Date: 22-Nov-1996 #sequence revision 22-Nov-1996 #text_change 05-Nov-1999
C;Accession: S65464; S65463; A54220; I38097
R;Haaning, J.; Oxvig, C.; Overgaard, W.T.; Ebbesen, P.; Kristensen, T.; Sottrup-Jensen, submitted to the EMBL Data Library, June 1995
A;Reference number: S65464
A;Reference number: S65464
A;Accession: S65464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: mRNA
A,Residues: 1-1677 < HRA-
A,Cross-references: EMBL:U28727; NID:g1142969; PIDN:AAC50543.1; PID:g1142970
A,Cross-references: EMBL:U28727; NID:g1142969; PIDN:AAC50543.1; PID:g1142970
R,Haaning, J.; Oxvig, C.; Overgaard, M.T.; Ebbesen, P.; Kristensen, T.; Sottrup-Jensen,
Bur. J. Biochem. 237, 159-163, 1996
A,Title: Complete cDNA sequence of the preproform of human pregnancy-associated plasma I
A,Reference number: S65463; MUID:96203921; PMID:8620868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: GDB:134729, OMIM:176385
A;Map position: 9q33.1-9q33.1
A;Map position: 9q33.1-9q33.1
F;1.22\Domain: signal sequence #status predicted <SIG>
F;23.80/Domain: propeptide #status predicted <PRO>
F;81-1627/Product: pregnancy-associated plasma protein A #status predicted <MAT>
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20914
R;Lloyd, C.
submitted to the EMBL Data Library, March 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 77-1627 <RES>
A;Cross-references: EMBL:X68280; NID:g394649; PIDN:CAA48341.1; PID:g394650
C;Genetics:
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Pred. No. 1.1e+02;
1; Mismatches 0; Indels
        Indels
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            Mismatches
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Best Local Similarity 83.3%;
Matches 5; Conservative
                Conservative
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                                                                                                                                                              123 ČIPĽÝČ 128
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A; Residues: 1-102 < HAW>
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Gaps

RESULT 4

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C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 17-Mar-2000
C;Accession: A53970
R;Emori, Y.; Sugaya, R.; Akimaru, H.; Higashijima, S.; Shishido, E.; Saigo, K.; Homma, Y. B. Biol. Chem. 269, 19474-19479, 1994
A;Title: Drosophila phospholipase C-gamma expressed predominantly in blastoderm cells at A;Reference number: A53970; MUID:94308233; PMID:8034716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Superfamily: 1-phosphatidylinositol-4, S-bisphosphate phosphodiesterase II; 1-phosphati hodiesterase domain Y homology; SH2 homology; SH3 homology C, Keywords: phosphoric diester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F,979-1095/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y ho
                                                                                                                                                                                                                                                                                                                   1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) gamma-D - fruit
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A;Molecule type: mRNA
A;Residues: 1-108 A:ERR>
A;Cross-references: GB:X53744; NID:g931; PIDN:CAA37774.1; PID:g933
C;Superfamily: dog hypothetical 12.2K protein (68K signal recognition particle region)
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F;589-688/Domain: SH2 homology <SH2B>
F;701-789/Domain: SH2 homology <SH2>
F;811-789/Domain: SH3 homology <SH3>
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           Length 650;
                                                                    1; Indels
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        Score 33; DB 2; I
Pred. No. 1.2e+02;
0; Mismatches 1;
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66.7%; Pred. No. 43;
iive 2; Mismatches
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A;Cross-references: FlyBase:FBgn0003416
        86.8%;
83.3%;
Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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Matches 5; Conserv
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Matches 4; Conserv
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20 CVPMSC 25
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                                                                                                                       1 CVPLTC
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T26433
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                                      transposase all4675 [imported] - Nostoc sp. (strain PCC 7120)
CiSpecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. pCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AC3390
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. B, 205-213, 2001
A;Aritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Accession: AC3390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable ethylene receptor - muskmelon
(Species: Cucumis melo (muskmelon)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C;Accession: T08050
R;Sato-Nara, K.; Yuhashi, K.; Higashi, K.; Hosoya, K.; Kubota, M.; Ezura, H.
submitted to the EMBL Data Library, December 1997
A;Description: Expression of an ERS homolog gene of melon (Cucumis melo L. reticulatus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein antigen Bm86 precursor - southern cattle tick (Species: Boophilus microplus (southern cattle tick) (cjbate: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 21-Jul-2003 (cjAccession: A34498 Proc. Matl. Acad. K.N.; Moore, T.; Sriskantha, A.; Spring, K.; Tellam, R.; Willadsen, P.; Cobon, A;Rand, K.N.; Moore, T.; Sriskantha, A.; Spring, K.; Tellam, R.; Willadsen, P.; Cobon, A;Title: Cloning and expression of a protective antigen from the cattle tick Boophilus A;Reference number: A34498; MUID:90099323; PMID:2690068
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A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: mRNA
A,Residues: 1-637 <SATS
A,Cross-references: EMBL:AF037368; NID:g2707333; PIDN:AAC99477.1; PID:g2707334
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Pred. No. 94;
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels
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C;Keywords: glycoprotein
F;209-246/Domain: EGF homology <EGF>
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A;Status: preliminary; translated from GB/EMBL/DDBJ

Reference number: 216317; Accession: T08050

86.8%;

Query Match
Best Local Similarity 83.3
Matches 5; Conservative

CVPYTC 231

226

RESULT A34498

1 CVPLTC 6

à g A;Residues: 1-650 <RAN>

A;Status: preliminary Molecule type: mRNA

0; Mismatches

86.8%; 83.3%;

Query Match 86.8 Best Local Similarity 83.3 Matches 5; Conservative

A;Gene: all4675

61 CCPLTC 66

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9

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-467 <KUR>

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Gaps

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Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Fas-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramee, E.E.; Laigned, J.B.; Martino, C.L.; Marques, M.V.; Martinos, E.M.F.; Matsukuma, A.Y.; March, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.; Kodrigues, V.; Rosa, A.J. de M., de Silva, V.E.; de Santelli, R.V.; Sawasa)
A;Authors: da Silva, A.C.R.; da Silva, A.M.; Silva, Jr., W.; Silva, M.M.; Silva, Jr., W.; da Silvei)
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
C;Genetics: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: response regulator with LytTR DNA-binding domain, AlgR/VirR/ComE type; r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 2; Length 252;
Pred. No. 86;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.2%; Score 32; DB 2; 66.7%; Pred. No. 1e+02; ive 1; Mismatches
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83.3%;
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Job time : 5.60606 secs
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T40593
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Cipate: 31-Nar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
CiAccession: C81364
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUD:20150912; PMID:10688204
A;Reference number: A81250; MUD:20150912; PMID:10688204
A;Reference speliminary
A,Molecule type: DNA
A;Residues: 1-156 <PAR>A;Residues: 1-156 <PAR>A;Residues: 0B:ALilling; NID:g6868128; PIDN:CAB73165.1; PID:g696834
A;Reperimental source: serotype 02, strain NCTC 11168
C;Genetics:
A;Gene: Cj0908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable periplasmic protein Cj0908 [imported] - Campylobacter jejuni (strain NCTC 11168 C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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                                                                                                                                                                                                                                                                                                                    A,Cross-references: EMBL:AL032631; PIDN:CAA21579.1; GSPDB:GN00019; CESP:Y106G6H.16
A,Experimental source: clone Y106G6H
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                      hypothetical protein Y106G6H.16 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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Pred. No. 58;
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                                                                                                    C)Accession: T26433
R:McMnray, A.
Submitted to the EMBL Data Library, October 1998
A;Reference number: 220214
A;Accession: T26433
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-137 <WIL>
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7
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0; Mismatches
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83.3%;
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A;Introns: 26/3; 61/3; 89/3
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A;Status: preliminary
A;Molecule type: DNA
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Gaps

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5.1.6	Compugen Ltd.
version	- 2004
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

September 5, 2004, 09:38:39; Search time 2.72727 Seconds (without alignments) 114.554 Million cell updates/sec Run on:

US-09-761-636A-12 38 1 CVPLTC 6 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		7 Pomod	ratti		, and	SVIDE						Dan	P50244 trypanosoma							homod	P59991 homo sapien	smint	~		~	_	Q7z407 homo sapien	bos t	o pos	soq e	4 bos	-	_
SUMMARIES	ID	CSM1 MOUSE	CSM1 HUMAN	PDP2_RAT	PAPA_HUMAN	CSM2_HUMAN	TPIS SYNEL	AA2B MOUSE	BM86_BOOMI				APOH_PANTR	DCAM_TRYBB	MUB1 XENLA	CHRD_BRARE	LMG3 MOUSE	LRP2 HUMAN	LRP2_RAT	BD05_BOVIN	K121 HUMAN	K122_HUMAN	OB_SMICR	V060_FOWPV	AVT_CATCO					BD02 BOVIN	BD07 BOVIN	1 1	BD09 BOVIN	BD03_BOVIN
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EAP_BOVIN LAP_BOVIN TAP_BOVIN KRUB HUMAN YK83_CAEEL DHSL HUMAN DHSL HUMAN BHSL MOUSE ETIR_RAT ETIR_RAT ETIR_HUMAN ETIR HUMAN
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# ALIGNMENTS

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RESULT 2

CSM1 HUMAN STANDARD; PRT; 3565 AA.

AC 096PZ7; Q96QU9; Q96RW4;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DG CUB and Sushi multiple domains protein 1 precursor (UNQ5952/PRO19863).

GN CSMD1 OR KTAA1890.

OS Homo sapiens (Human).
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Pred. No. 41;
1; Mismatches 0; Indels
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Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CUB AND SUSHI MULTIPLE DOMAINS PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sushi; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. CYTOPLASMIC (POTENTIAL)
                                                                                                                       Isold=Q923L3-3; Sequence=VSP_009036;
Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the CSMD family.
-!- SIMILARITY: Contains 14 CVB domains.
-!- SIMILARITY: Contains 28 Sushi (SCR) domains.
                                                               Name=2;
IsoId=Q923L3-2; Sequence=VSP_009037;
Note=No experimental confirmation available;
                  Event=Alternative splicing; Named isoforms=3;
                                                  IsoId=Q923L3-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                 EMEL; AY017475; AAGS4083.1; -.
EMEL; AX038679; BAG30095.1; ALT_INIT.
EMBL; AK082377; BAG38482.1; -.
MGD; MGI.2137383; CSmdl.
InterPro; IPR000859; CUB.
InterPro; IPR00436; Sushi_SCR_CCP.
Pfam; PF00431; CUB; 14.
Pfam; PF00431; CUB; 14.
Pfam; PF00184; Sushi; 28.
SMART; SM00032; CCP; 28.
SMART; SM00042; CUB; 14.
PROSITE; PS01180; CUB; 14.
Repeat; Signal; Transmembrane; Sushi; A
SIGNAL
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       ALTERNATIVE PRODUCTS:
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Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatua M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain,
MEDLINE=21456161; PubMed=11572484;
Nagase T., Kikuno R., Ohara O.;
Nagase T., Kikuno R., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XXI.
"Prediction of the complete sequences of 60 new cDNA clones from brain which code for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toomes C., Jackson A., Maguire K., Wood J., Gollin S., Ishwad C., Paterson I., Prime S., Parkinson K., Bell S., Woods G., Markham A., Oliver R., Woodward R., Sloan P., Dixon M., Read A., Thakker N.; "The presence of multiple regions of homozygous deletion at the CSMD1 locus in oral squamous cell carcinoma question the role of CSMD1 head and neck carcinogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-22887296; PubMed=12975309;
Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J.,
Clark H.F., Gurney A.L., Crowley C., Currell B., Deuel B., Dowd P.,
Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M. Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

MEDLINE=21365705; PubMed=11472063;

Sun P.C., Uppaluri R., Schmidt A.P., Pashia M.E., Quant E.C.,
Sunwoo J.B., Gollin S.M., Scholnick S.B.;

"Transcript map of the 8p23 putative tumor suppressor region.";
Genomics 75:17-25(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Potential suppressor of squamous cell carcinomas.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=4;
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IsoId=096P27-2; Sequence=VSP_009034, VSP_009035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSP 009031;
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Scholnick S.B., Richter T.M.;
"The role of CSMD1 in head and neck carcinogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note=No experimental confirmation available;
                                                                                                                                                                                                                       SEQUENCE OF 1319-3565 FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes Chromosomes Cancer 38:281-283(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22581359; PubMed=12696061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bioinformatics assessment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   large proteins.";
NA Res. 8:179-187(2001).
                                      NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
           -!- TISSUE SPECIFICITY: Weakly expressed in most tissues, except in brain. Expressed at intermediate level in brain, including cerebellum, substentia nigra, hippocampus and fetal brain.
-!- DISEASE: Defects in CSMD1 may be a cause of oral and oropharyngeal squamous cell carcinomas (OSCCs). Ref.5 and Ref.6 are however in disagreement: while Ref.6 considers CSMD1 as a strong candidate for OSCCs, Ref.5 thinks it is not.
-!- SIMILARITY: Belongs to the CSMD family.
-!- SIMILARITY: Contains 14 CUB domains.
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IsoId=Q96PZ7-4; Sequence=VSP_009032, VSP_009033;
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SUSHI 15.
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InterPro: IPR000859; CUB.
InterPro: IPR000485; Sushi_SCR_CCP.
Pfam; PF00431; CUB; 14.
Pfam; PF00084; Sushi; 27.
SWART; SM00042; CUB; 14.
PROSITE; PS01180; CUB; 14.
ROSITE; PS01180; CUB; 14.
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EMBL, AX12635, BAC68754.1, ALT INIT.
EMBL, AY58174; AAQ8854.1; ALT_INIT.
EMBL, A8067477; BAB67783.1; -.
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Eur. J. Biochem. 237:159-163(1996)
        MEDLINE=98316337; PubMed=9651365;
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InterPro; IPR001932; PP2C-like.
InterPro; IPR000222; PP2C.
Ffam; PF00481; PP2C; 2.
SMART; SM00331; PP2C SIG; 1.
SMART; SM00332; PP2CC; 1.
PROSITE; PS01032; PP2C; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation updatas)
19-vouvate dehydrogenase [Lipoamide]]-phosphatase 2, mitochondrial
precursor (EC 3.1.3.43) (PDP 2) (Pyruvate dehydrogenase phosphatase,
catalytic subunit 2) (PDPC 2).
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ALMULIARE-9311039; FULDWEGE=2051205;
THURING BY, GODI R., Wu P., Harris R.A., Hamilton J., Popov K.M.;
Huang B., Godi R., Wu P., Harris R.A., Hamilton J., Popov K.M.;
Tisoenzymes of pyruvate dehydrogenase phosphatase. DNA-derived amino
Total sequences, expression, and regulation.";
Total States and regulation.";
The states of the alpha subunit of the BI component of the Pyruvate dehydrogenase complex.
Tractivation of the alpha subunit of the BI component of the pyruvate dehydrogenase complex.
The CAPALYTIC ACTIVITY: [Pyruvate dehydrogenase (lipoamide)] + phosphate.
TOTACTOR: Magnesium.
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MEDLINE=96203921; PubMed=8620868;
MEDLINE=96203921; PubMed=8620868;
Haaning J., Oxvig C., Overgaard M.T., Ebbesen P., Kristensen T.,
Sottrup-Jensen L.;
"Complete cDNA sequence of the preproform of human pregnancy-
associated plasma protein-A. Evidence for expression in the brain and
induction by CAMP.";
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Hydrolase; Micchondrion; MITCHONDRION (POTENTIAL).
CHAIN 68 530 [PYROYATE DEHYDROGENASE [LIPOAMIDE]].
SEOUBNCE 530 AA, 59654 MW, SAB688FAC78AD9CD CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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"Expression of recombinant human pregnancy-associated plasma protein-A and identification of the proform of eosinophil major basic protein as its physiological inhibitor.";
J. Biol. Chem. 275:31128-31133(2000).
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"Circulating human pregnancy-associated plasma protein-A is disulfide-
bridged to the proform of eosinophil major basic protein.";
J. Biol. Chem. 268:12243-12246(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99179030; PubMed=10077652; Lawrence J.B., Oxvig C., Overgaard M.T., Sottrup-Jensen L., Gleich G.J., Hays L.G., Yates J.R. III, Conover C.A.; "The insulin-like growth factor (IGF)-dependent IGF binding protein-4 protease secreted by human fibroblasts is pregnancy-associated plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95057018; PubMed=7526035; Bonno M., Oxvig C., Kephart G.M., Wagner J.M., Kristensen T., Sottrup-Jensen L., Gleich G.J.; "Localization of pregnancy-associated plasma protein-A and colocalization of pregnancy-associated plasma protein-A messenger ribonucleic acid and eosinophil granule major basic protein messenger ribonucleic acid in placenta."; ribonucleic acid in placenta."; Lab. Invest. 71:560-566(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Overgaard M.T., Sorensen E.S., Stachowiak D., Boldt H.B.,
Kristensen L., Sottrup-Jensen L., Oxvig C.,
"Complex of pregnancy-associated plasma protein-A and the proform of
eosinophil major basic protein. Disulfide structure and carbohydrate
attachment sites.";
J. Biol. Chem. 278:2106-2117(2003).
                     SEQUENCE OF 77-1627 FROM N.A., SEQUENCE OF 81-98; 117-126; 210-224; 466-485; 507-519; 576-593; 609-621; 718-736; 742-754; 1006-1017; 1259-1273; 1359-1374; 1389-1398; 1490-1509; 1524-1533 AND 1537-1544, VARLANT SER-944, AND TISSUE SPECIFICITY.
                                                                                                                                             Kristensen T., Oxvig C., Sand O., Moller N.P.H., Sottrup-Jensen L., "Amino acid sequence of human pregnancy-associated plasma protein-A derived from cloned cDNA.";

Biochemistry 33:1592-1598(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
MEDLINE=22421368; PubMed=12421832;
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MEDLINE=99423540; PubMed=10491647;

Overgaard M.T., Oxvig C., Christiansen M., Lawrence J.B.,

Conover C.A., Gleich G.J., Sottrup-Jensen L., Haaning J.;

"Messenger ribonucleic acid levels of pregnancy-associated plasma protein—A and the profform of ecainophil major basic protein:

expression in human reproductive and nonreproductive tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20469470; PubMed=10913121;
Overgaard M.T., Haaning J., Boldt H.B., Olsen I.M., Laursen L.S.,
Christiansen M., Gleich G.J., Sottrup-Jensen L., Conover C.A.,
                                                                                                                                                                                                                                                                     718-736; 742-754; 1259-1273; 1369-1374; 1490-1509; 1524-1533 AND 1537-1544, SUBUNITS, AND INTERCHAIN DISULFIDE BOND.
                                                                                                                                                                                                                                              SEQUENCE OF 81-89; 117-126; 210-224; 460-485; 507-519; 576-593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 96:3149-3153(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION, SUBUNITS, AND ENZYME REGULATION.
                                                                                                                                                                                                                                                                                                                             MEDLINE=93286045; PubMed=7685339;
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DEVELOPMENTAL STAGE
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SEQUENCE OF
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 of PRG2.

-1- SUBGNIT: Homodimer; disulfide-linked In pregnancy serum, predominantly found as a disulfide-linked 2:2 heterotetramer with the proform of PRG2.
-1- SUBCELDUAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: High levels in placenta and pregnancy serum.
-1- TISSUE SPECIFICITY: High levels in placenta and anchoring villi, and in syncytiotrophoblasts in the chorionic villi. Lower levels are found in a variety of other tissues including kidney, comyometrium, endometrium, ovaries, breast, prostate, bone marrow, colon, fibroblasts and osteoblasts.
-1- DEVELOPMENTAL STAGE: Present in serum and placenta during pregnancy; levels increase throughout pregnancy.
-1- INDUCTION: By * b-bromoadenosine-3', 5'-phosphare.
-1- INDUCTION: By * B-bromoadenosine-3', 5'-phosphare.
-1- INDUCTION: By * B-bromoadenosine-3', 5'-phosphare.
-1- FPM: There appear to be no free sulfhydryl groups.
-1- SIMILARITY: Belongs to peptidase family M43B.
Oxvig C., Haaning J., Kristensen L., Wagner J.M., Rubin I., Stigbrand T., Gleich G.J., Sottrup-Jensen L.;
"Identification of angiotensinogen and complement C3dg as novel proteins binding the proform of eosinophil major basic protein in human pregnancy serum and plasma.";
J. Baol. Chem. 270:13645-13651(1995).
-! FUNCTION: Metalloproteinase which specifically cleaves IGFBP-4 in the presence of IGF, resulting in release of bound IGF.
-!- CATALYTIC ACTIVITY: Cleavage of the 135-Met. |-Lys-136 bond in insulin-like growth factor binding protein (IGFBP)-4, and the 143-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metal-binding; Zinc; Signal; Glycoprotein;
                                                                                                                                                                    Ser-|-Lys-144 bond in IGFBP-5.
COFACTOR: Binds 1 zinc ion per subunit (By similarity).
ENZYME REGULATION: Inhibited by complexation with the proform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO: 0008576; C: extracellular; IDA.
GO; GO: 0008277; F: metallopeptidase activity; IDA.
GO; GO: 0008277; F: metallopeptidase activity; IDA.
GO; GO: 0007565; P: pregnancy; NAS.
InterPro; IPR008985; ConA like lec_gl.
InterPro; IPR008985; ConA like.
InterPro; IPR008080; Notch dom.
InterPro; IPR008075; Pept M Zn BS.
InterPro; IPR008075; Pept M Zn BS.
InterPro; IPR00815; Pept M Zn BS.
InterPro; IPR00816; Sushi SCR CCP.
Ffam; PF00587; Peptidase_M46; I.
SMART; SM0052; CCP; 4.
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PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Metal-b
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Genew; HGNC:8602; PAPPA.
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Submitted (JUL-2003)
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SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 2969-3487 (ISOFORM 1).

TAISSUB-Brain, and Teratocarcinoma;

TaisSUB-Brain, and Teratocarcinoma;

TaisSub-Brain, Enjamara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,

Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,

Isono Y., Kawain H., Sato H., Wakamateu A., Ishii S., Yamamoto J.,

Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Magatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,

Sugiyama A., Kawakami T.,

"NEDO human cDNA sequencing project.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                         PRG2 PROFORM)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSM2 HUMAN STANDARD; PRT; 3487 AA.

GYZ406 QR086; Q9H4W0; Q9H4W1; Q9H4W1; Q9H4W1; Q9H4W3; Q9H4W3; Q9H4W3; Q9H4W3; Q9H4W3; Q9H4W3; Q9HCY5; Q9HCY7; Q9HCY7; G9H4W3; Q9H4W3; Q9HCY5; Q9HCY7; G9HCY7; G9HC
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           ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 1; Length 1627; Pred. No. 30;
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OR 587-600.
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5; Conservative 1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                            MEDINEEZEBREZE, PUDNEG=124/932,
A Strausberg R.L., Feingod E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Feingod E.A., Grouse L.H., Derge J.G.,
A Strausberg R.L., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hateh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J. Usdin T.B., Tonshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarane P.H.,
Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunzarane P.H.,
A Richards S., Worley K.C., Sheoria A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muany D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. Cherch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note=No experimental confirmation available;
-!- TISSUE SPECIFICITY: Weakly expressed in most tissues, except in brain. Expressed at intermediate level in brain, including cerebellum; substantia nigra, hippocampus and fetal brain. Overexpressed in some head and neck cancer cell lines.
-!- SIMILARITY: Belongs to the CSMD family.
-!- SIMILARITY: Contains 14 CUB domains.
-!- GIMILARITY: Contains 26 Sushi (SCR) domains.
-!- CAUTION: Ref. 3 sequence differs from that shown due to a frameshift in position 939 that shortens the protein by 1021 residues in its N-terminus. It is unknown whether the sequence shown exists or whether Ref. 3 is right, shortening the sequence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagase T., Kikuno R., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XXI.
The complete sequences of 60 new cDNA clones from brain which code for
large proteins.";
DNA Res. B:179-187(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAUTION: Ref.3 sequence differs from that shown due to erroneous gene model prediction.
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the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Name=2;
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                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 3).
         to
                                                                                                                                 Wallis J., Brown A.;
Submitted (SEP-2000)
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                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphate.
-!- PATHWAY: Plays an important role in several metabolic pathways.
-!- SUBUNIT: Homodimer (By similarity).
-!- SIMILARITY: Belongs to the triosephosphate isomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=2225144; PubMed=12240834; MEDLINE=2225144; PubMed=12240834; MEDLINE=2225144; PubMed=12240834; Maramura Y., Kaneko T., Sato S., Ikeuchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Marsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermosphilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
                                                                                                                                                                                                                                                                                                                                      Score 35; DB 1; Length 3487;
Pred. No. 63;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MRR-2004 (Rel. 43, Created)
15-MRR-2004 (Rel. 43, Last sequence update)
15-MRR-2004 (Rel. 43, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
Triosephosphate isomerase (EC 5.3.1.1) (TIM).
TPIA OR TPI OR TLR0966.
Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chrococccales; Synechococcus.
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ilarity 83.3%;
Conservative
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TPIS SYNEL
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( HSSP; P10998; IVVD.

R Genew; HGNC:19290; CSMD2.

R InterPro; IPR000436; Sushi_SCR_CCP.

DR InterPro; IPR000436; Sushi_SCR_CCP.

DR Pfam; PF00041; CUB; 14.

DR SMART; SM00032; CCP; 26.

DR SMART; SM00042; CUB; 14.

DR PCSITE; PS01180; CUB; 14.

DR PCSITE; PS01180; CUB; 14.

RWAIN; Repeat; Transmembrane; Sushi; Alternative splicing.

NMAIN; 2409 3429 POTENTIAL.

TANDALINE (POTENTIAL).

CTT. 1.
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CUB 3.
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AK095627; E
AK127722; E
                                                   AC115286;
AL121980;
AL121980;
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AL355178;
AL355178;
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AL355178;
                                     AC115285;
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Query Match
Best Local Similarity 85...
5; Conservative
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"Cloning of two adenosine receptor subtypes from mouse bone marrow-derived mast cells.", 152:4508-4515 (1994).
-: FUNCTION: Receptor for adenosine. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase.
-: SUBCELLULAR LOCATION: Integral membrane protein.
-: SUBCELLULAR Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                            pfam; PF00121; TIM; 1.
ProDom; PF001025; Triophoa ismrse; 1.
TIGREAMs; TIGR00419; Lim; 1.
PROSITE; PS00171; TIM; 1.
Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis; Pentose shunt; Complete proteome.
ACT_SITE | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 118 | 11
                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                          Length 265;
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PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein coupled are EXTRACELLULAR (POTENTIAL).
DOMAIN 1 1 (POTENTIAL).
DOMAIN 32 44 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
; 92A0D6015B51927A CRC64;
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                          86.8%; Score 33; DB 1;
83.3%; Pred. No. 12;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (POTENTIAL).
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          InterPro; IPR000652; Triophos_ismrse.
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InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PFINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/c; TISSUE=Bone marrow; MEDLINE=94209670; PubMed=8157966;
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                                                                                                                                                                          118 118 BY
187 187 BY
265 AA; 29096 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U05673; AAA19001.1; -. PIR; 148933; I48933.
HSSP; P29274; IMMH.
                                                                                                                                                                                                                                                                                                    Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                            1 CVPLTC 6
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Q60614;
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MEDLINE=90099323; PubMed=2690068;
Rand K.N., Moore T., Sriskantha A., Spring K., Tellam R.L.,
Willadsen P., Cobon G.S.;
"Cloning and expression of a protective antigen from the cattle tick
Boophilus microplus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF 1; FALSE_NEG.
PROSITE; PS01186; EGF 2; FALSE_NEG.
Glycoprotein; Antigen; Signal; EGF-like domain; Repeat; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Willadsen P., Riding G.A., McKenna R.V., Kemp D.H., Tellam R.L., Nielsen J.N., Lahnstein J., Cobon G.S., Gough J.M., Inhunologic control of a parasitic arthropod. Identification of a protective antigen from Boophilus microplus."; J. Immunol. 143:1346-1351(1989).

-: SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
S-palmitoyl cysteine (Potential).
C8A3108371AD1C1C CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1993 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
61ycoprotein antigen BMS6 precursor (Protective antigen).
Boophilus microplus (Cattle tick).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Boophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1; Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                               EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                           7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 86:9657-9661(1989).
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-!- SIMILARITY: Contains 7 EGF-like domains.
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                                                                                                                                                                                                                             BY SIMILARITY.
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                                                                                         6 (POTENTIAL)
                               5 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE.
MEDLINE-89309823; PubMed=2745982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A34498; A34498.
InterPro; IPR006209; EGF like.
InterPro; IPR065210; IEGF.
PFam; PF00008; EGF; 2.
SMART; SM00181; EGF; 2.
                                                                                                                                                                                                                                                                                                                                                                    36064 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     86.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.3%;
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RL J. Cell Biol. 145:605-618(1999).

CC :- FUNCTION: Binding to cells via a high affinity receptor, laminin of is thought to mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.

CC :- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globules at each end rang man-3 chain is a subunit of laminin-12.

CC :- SUBCELLULAR LOCATION: Extracellular.

CC :- DOMAIN: The alpha-helical domains I and II are thought to interact convict the reproductive tracts.

CC :- DOMAIN: The alpha-helical domains of structure.

CC :- SUMILARITY: Contains I laminin N-terminal domains.

CC :- SIMILARITY: Contains I laminin IV domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein, Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
SIGNAL 1 19 POTENTIAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAMININ GAMMA-3 CHAIN.
LAMININ GAMMA-3 CHAIN.
LAMININ BGF-LIKE 1.
LAMININ BGF-LIKE 2.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 4.
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 6.
LAMININ BGF-LIKE 6.
LAMININ BGF-LIKE 6.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 9.
LAMININ BGF-LIKE 9.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 601349; AMINIO, 601349; AMINIO, 601349; AMINIO, 601349; C:extracellular matrix; TAS.

GO; GO:0016020; C:membrane; TAS.

GO; GO:0016020; C:membrane; TAS.

GO; GO:0016020; C:membrane; TAS.

R InterPro; IPR006212; Lam N2.

InterPro; IPR00231; Laminin B.

R InterPro; IPR00249; Laminin B.

R InterPro; IPR00249; Laminin B.

R Pfam; PF00052; laminin BF; J.

Pfam; PF00055; laminin BF; J.

R PRNUTS; PR00011; EGFLIMIN.

R PROSTIE; SM00180; EGF Lam; J.

R PROSTIE; PS00186; EGF Lam; J.

R PROSTIE; PS00186; EGF Lin; J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN II AND I.
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                  GLYCOPROTEIN ANTIGEN BM86.

(BY SIMILARITY).

(BY SIMILARITY).

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 4.

EGF-LIKE 5.

EGF-LIKE 6.

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MEDLINE-99242614; PubMed=10225960;
MEDLINE-99242614; PubMed=10225960;
Koch M., Olson P.F., Albus M.P.,
Burgeson R.E., Champlaud M.F.;
"Characterization and expression of the laminin gamma3 chain: a novel, non-basement membrane-associated, laminin chain.";
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 30;
0; Mismatches 1; Indels
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15-MAR-2004 (Rel. 43, Last annotation update)
Laminin gamma-3 chain precursor (Laminin 12 gamma 3).
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N-LINKED (GLCNAC.
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N-LINKED (GLCNAC.
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28-FEB-2003 (Rel. 41, Last seq
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83.3%;
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Matches 5; Conservative
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650 AA;
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SEQUENCE FROM N.A.
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15-MAR-2004
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HUMAN
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263
268
271
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263
268
271
302
314 AA;
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258 CIPLAC 263
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=Liver;
                                                          Query Match
Best Local Similarity
                                                                                                 CVPLTC 6
                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
                             METAL
SEQUENCE
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APOH BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                         Brunel F., Davison J.;
"Cloning and sequencing of Pseudomonas genes encoding vanillate demethylase.";
J. Bacteriol. 17. 170:4924-4930(1988).
-!- COFACTOR: FMN (By similarity).
-!- PATHWAY: Vanillate degradation (vanillate is a key intermediate in the degradation of lignin).
-!- SIMILARITY: Belongs to the PDR/vanB family.
-!- SIMILARITY: In the C-terminal section; belongs to the 2Fe2S plant-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfenn; PP00175; NAD binding 1; 1.
PRINTS; PR00409; PHDIOXRDTASE.
PR051TE; PS0191; 2FEZS_FERREDOXIN; 1.
Aromatic hydrocarbons catabolism; Lignin degradation; Oxidoreductase; Flavoprotein; FMN; NAD; Metal-binding; Iron-sulfur; Iron; 2Fe-2S;
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                      01-007-1989 (Rel. 12, Created)
01-007-1989 (Rel. 12, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Vanillate O-demethylase oxidoreductase (EC 1.14.13.-) (Vanillate
                                                                       (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
                                           (POTENTIAL)
                                                             (POTENTIAL)
                                 (POTENTIAL)
                                                                                                                                            ..
0
                      (POTENTIAL)
             (POTENTIAL)
     ATTACHMENT SITE (POTENTIAL)
                                                                                                                       DB 1; Length 1587;
                                                                                                                                           1; Indels
                                                                                                    MW; 3CB6E09B5F203319 CRC64;
                                                    (GLCNAC. . .)
                                                                                 (GLCNAC. . .)
                                  (GLCNAC. . .)
                                            (GLCNAC. . .)
                                                                        (GLCNAC. . .)
                                                                                                                                             Mismatches
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InterPro; IPR008333; FAD_binding_6.
InterPro; IPR001041; Perredoxin.
InterPro; IPR001433; Oxred_FAD/NAD(P).
InterPro; IPR000951; Phdiox reductase.
Pfam; PF00970; FAD_binding_6; 1.
Pfam; PF00111; Fer2; 1.
                                                                                                                         Score 33;
Pred. No.
    CELL ATTAC
N-LINKED
                                                                                                                                                                                                                                                                                               degradation ferredoxin-like protein)
                                                                                                                                                                                                                                                                                                                  Pseudomonas sp. (strain ATCC 19151).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FMN.
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HSSF; P33164; 2PIA.
                                                                                                                        86.8%;
                                                                                                      172051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type ferredoxin family.
                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria.
                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                     STANDARD;
                                                                        980
1185
1518
                                                                                                      AA;
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                                                                                                                                                                                   704 CVPCTC 709
                                                                                                                                 Local Similarity
                                                                                                                                                                 1 CVPLTC 6
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                        119
295
328
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P12580;
                        CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 20-345, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
TISSUB=Plasma;
MEDLINE=92089075; PubMed=1751487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kato H., Enjyoji K.-I.;
"Amino acid sequence and location of the disulfide bonds in bovine
beta 2 glycoprotein I: the presence of five Sushi domains.";
Biochemistry 30:11687-11694(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 4-345 FROM N.A., PARTIAL SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APOH BOVIN STANDARD; PRT; 345 AA.
17450/ 228052;
01-AUG-1990 (Rel. 15, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
(Beta(2)GPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
(BY SIMILARITY).
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Appella E., Kunos G., Takacs L.,
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete primary structure of bovine beta 2-glycoprotein localization of the disulfide bridges."; Biochemistry 31:3611-3617(1992).
                                                                                                                                                          Score 32; DB 1; Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bendixen E., Halkier T., Magnusson S., Sottrup-Jensen L.,
Kristensen T.;
                                                                                                                                                                                                             1; Indels
                                                                                                            FC521516AA6CEB72 CRC64;
  IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
IRON-SULFUR (2FE-2S) (
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                                                                                                                                                                                  Pred. No. 23;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 20-41.
MEDLINE=90226328; PubMed=2327984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92232647; PubMed=1567819;
                                                                                                            33706 MW;
                                                                                                                                                               84.2%;
                                                                                                                                                                                                                   4; Conservative
                                                                                      302
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"Chimpanzee apolipoprotein H (beta2-glycoprotein I): report on the
                                                                                                                                                                                                                                                                                                                                                                                                                      1 CVPLTC 6
                                                                                                                                                                                                                    Polymorphism.
SIGNAL
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SEQUENCE
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  removed. Usage by and for commercial ant (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Beta-2-glycoprotein I precursor (Apolipoprotein H) (Apo-H) (B2GPI)
(Beta(2)GPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                           ..
                                                                       Heparin-binding; Glycoprotein; Plasma; Repeat; Sushi; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] —
SEQUENCE FROM N.A., AND VARIANT GLU-229.
MEDLINE=21372074; PubMed=11479737;
Sanghera D.K., Nestlerode C.S., Ferrell R.E., Kamboh M.I.;
                                                                                                                                                                                                                                                                                                             DB 1; Length 345;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                               E117DAB609461C33 CRC64;
                                                                                     BETA-2-GLYCOPROTEIN I
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S (IN REF 1)

N (IN REF 1)

C (IN REF 1)

O (IN REF 1)

N (IN REF 1)

N (IN REF 1)

N (IN REF 1)

N (IN REF 1)

R (IN REF 1)
                                                                                                                                                                                                                 (GLCNAC.
                                                                                                                                                                                                                             (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                    345 AA
                                                                                                                                                                                                                                                                                                           84.2%; Score 32; DB 66.7%; Pred. No. 26; ive 1; Mismatches
      entities requires a license agreement (sor send an email to license@isb-sib.ch).
                                                                                                                      SUSHI-LIKE
                                                                                                                                                                                                           N-LINKED
N-LINKED
                                                                                                                                                                                                                      N-LINKED
N-LINKED
                        EMBL; L07303; AAA30382.1; -.
EMBL; X60065; CAA42669.1; -.
P.R.; JM0502; NBBO.
HSSP; P02749; 1C1Z.
InterPro; IPR000416; Sushi_SCR_CCP.
Pfam; PF00084; sushi; 4.
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modified and this statement is not
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15-MAR-2004 (Rel. 43, Last sequ
15-MAR-2004 (Rel. 43, Last ann
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gene structure, a common polymorphism, and a high prevalence of antiphospholipid antibodies.";

Hum. Genet. 109:63-72(2001).

-!- FUNCTION: Binds to various kinds of negatively charged substances such as heparin, phospholipids, and dextran sulfate. May prevent activation of the intrinsic blood coagulation cascade by binding to phospholipids on the surface of damaged cells.

-!- SUBCELLULAR LOCATION: Secreted (By similarity).

-!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.

-!- SIMILARITY: Contains 4 Sushi (SCR) domains.
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BETA-2-GLYCOPROTEIN I.
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N-LINKED (GLCNP.
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(Rel. 34, Last sequence update)
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Pred. No.
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EMBL; AF358408; AAK71538.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF358409, AAX71538.1; JOINED.
EMBL, AF358410; AAX71538.1; JOINED.
EMBL, AF358411; AAX71538.1; JOINED.
EMBL, AF358412; AAX71538.1; JOINED.
EMBL, AF358413; AAX71538.1; JOINED.
EMBL, AF358414; AAX71538.1; JOINED.
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Pfam; PF00084; sushi; 4.
SMART; SM00032; CCP; 4.
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Best Local Similarity
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DCAM TRYBB
ID DCAM TRYBB
AC P50244;
DT 01-0CT-1996 (;
DT 01-0CT-1996 (;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermidine biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen.
CHAIN 1 85 S-ADENOSYLMETHIONINE DECARBOXYLASE BETA
CHAIN (BY SIMILARITY).
CHAIN 86 370 S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA
                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                     S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50) (AdoMetDC) (SamDC) [Contains: S-adenosylmethionine decarboxylase alpha chain; S-adenosylmethionine decarboxylase beta chain].
Trypanosoma brucei brucei.
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                                                                                                                                                                                                                                                                   Trypanosoma brucei.";
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-adenosyl) (3-aminopropyl) methylsulfonium salt + CO(2).
-!- COFACTOR: Pyruvoyl group.
-!- PATHMAY: Decarboxylation of S-adenosylmethionine provides the aminopropyl moiety required for spermidine and spermine biosynthesis from putrescine.
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                                                                                                                                                                                           STRAIN-BATRO 164;
Scott J.R., Ullman B.;
"Molecular cloning and functional expression of the S-
adenosylmethionine decarboxylase gene of Leishmania donovani and
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CLEAVAGE (NONHYDROLYTIC)

CLEAVAGE (NONHYDROLYTIC)

CONVERTED TO A PYRUVOYL GROUP
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01-0CT-1994 (Rel. 30, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
11-0CT-2003 (Rel. 42, Last annotation update)
Nenopus laevis (African clawed frog).
      Last annotation update)
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Pfam; PF01536; SAM decarbox; 1.
Prothom; P0012379; SAM decarbox; 1.
TICRFAMS; TICR00535; SAM DCame; 1.
PROSITE; PS01336; ADOMETDC; 1.
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P38565;
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0
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Biochemistry 29:62440-6244 [1990].

-i. FUNCTION: Could be involved in defense against microbial infections. Protects the epithelia from external environment.

-i. SUBCELLUIAR LOCATION: Secreted.

-i. TISSUE SPECIFICITY: Expressed and stored exclusively in mature mucous glands of the skin.

-i. PTM: Extensively 0-Glycosylated.

-i. SIMILARITY: Contains 1 VWFC domain.

-i. SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
                                                                                               SEQUENCE FROM N.A.
MEDLINE=91002513; PubMed=2207068;
Probst J.C., Gertzen E.-M., Hoffmann W.;
Probst J.C., Gertzen E.-M., Hoffmann W.;
"An integumentary mucin (FIM-B.1) from Xenopus laevis homologous with von Willebrand factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Pred. No.
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InterPro; IPR006208; Cys knot.
InterPro; IPR006207; Cys knot.
InterPro; IPR001007; VWP_C.
Pfam; PP00007; Cys knot; 1.
SMART; SM00041; CT_ 1.
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BY
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62
76
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1 93
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Best Local Similarity
'.hea 5; Conserve
                                                Kenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                    NCBI_TaxID=8355;
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PEQUENCE OF 1-42 FROM N.A.

Record of the control o
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                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                   "Differential regulation of chordin expression domains in mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VWFC 2.
VWFC 3.
VWFC 4.

N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                               TISSUE=Gastrula;
MEDLINE=88104254; PubMed=9441687;
Miller-Bertoglio V.E., Fisher S., Sanchez A., Mullins M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the chordin family. SIMILARITY: Contains 4 CHRD domains. SIMILARITY: Contains 4 WWFC domains.
057472; Q9DED8;
16-OCT--2001 (Rel. 40, Created)
16-OCT--2001 (Rel. 40, Last sequence update)
10-OCT--2003 (Rel. 42, Last annotation update)
Chordin precursor (Chordino protein).
                                                                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CHORDIN.
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CHRD 1.
CHRD 2.
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PROSITE; PS01208; VWFC 1; 3.
PROSITE; PS50184; VWFC 2; 4.
Developmental protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF034606; AAB93485.1; -.
EMBL; AB043968; BAB18642.1; -.
ZFIN; ZDB-GENE-990415-33; chd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dev. Biol. 192:537-550(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006559; SGG,
InterPro; IPR001007; VWF_C.
Pfam; PF00093; VWC; 4.
SMART; SM00566; SGG; 3.
SMART; SM00214; VWC; 4.
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748
836
919
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Query Match
B4.2%; Score 32; DB 1; Length 940;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps
Qy 1 CVPLTC 6
Db 815 CPPLTC 820
Search completed: September 5, 2004, 09:56:09
Job time: 3.7272 secs
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104999 MW; B855CAF84F4623AC CRC64;

940 AA;

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US-09-761-636A-12 38 1 CVPLTC 6 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL\_25:\*
1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_tungi:\*
4: sp\_tungi:\*
5: sp\_invertebrate:\*
5: sp\_mannal:\*
6: sp\_mannal:\*
6: sp\_mhc:\*
7: sp\_phage:\*
7: sp\_phage:\*
7: sp\_phage:\*
7: sp\_phage:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. plant:
sp\_blant:
sp\_rodent:\*
sp\_virus:\*
sp\_vortebrate:\*
sp\_vortebrate:\*
sp\_virus:\*
sp\_bacteriap:\*
sp\_archeap:\*

		Description	O963e7 caenorhabdi	Olasanorhabdi	07skg4 himan immin	O9h4w4 homos anies	notices omore support	090313 ming minging.	Ogfrmd homo canion	Ogdomo hrachidanio	Ogika miscuito	OBOTOWS mile miscuria	Ogens musculus	Obecok mis miscalli	O874k9 mis misculu	OBr4k7 mus musculu	O77408 homo sanion	Q8h347 oryza sativ	
SUMMARIES		αī	Q963E7	018280	Q7SKG4	O9H4W4	600960	092313	096RM4	09DGM2	09JK57	OB0VW3	096003	09ES06	08R4K8	08R4K7	072408	Q8H347	
		BB	Z,	Ŋ	15	4	4	11	4	13	11	11	4	11	11	11	4	10	
		Watch Length DB	447	447	849	533	3389	3564	3566	426	468	578	946	1367	1545	1574	3487	152	
ov	Query	Match	97.4	97.4	97.4	94.7	94.7	94.7	94.7	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	89.5	
		Score	37	37	37	36	36	36	36	35	35	35	35	35	35	35	35	34	
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081ku4 sorghum bic	O9xu36 caenorhabdi	O882a0 orvza sariv	OSDBES DOWN Sanien	O9Dtm2 coturnix co					C	O8dka0 synechocococ		D9lid1 arabidonais		xenopus	Yenonis		ORVINGS analyses on		ũ		O9v0v1 hoophilms m	OBWS87 hvalomma an	ORITES himan immin	ORIJS4 himan immin	OBimOn nlasmodium	090zn3 callus call		
QBLKU4	09XU36	08S2A0	QBN9T9	Q9PTM2	09A1P4	Q9PTM3	078161	Q90YB8	Q95YD9	Q8DKA0	09PYV4	09LID1	091548	07ZX05	091650	OBMOR1	OBYN93	O7YZB6	O9SSY5	049077	Q9Y0V1	08WS87	08UL55	08UL54	08IM00	090ZN3	Q9VXH3	Q24284
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245	367	511	570	99	99	68	93	168	246	265	277	395	415	415	429	443	467	556	637	637	650	664	852	852	875	1007	1230	1230
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34	34	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

1	Q963E7 PRELIMINARY; PRT; 447 AA.	01-DEC-2001 (TrEMBLyre) 19 Created)	(TrEMBLrel. 19,	25,	3UR-3	GUR-3.	Caenorhabditis elegans.	Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea	Rhabditidae; Peloderinae; Caenorhabditis.	NCBI_TaxID=6239;	SEQUENCE FROM N.A.	Robertson H.M.;	"Gustatory related receptors in nematodes.":	Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases	AAK70489.1;	GO; GO:0016020; C:membrane; IEA.	); GO:0005549; F:odorant binding; IEA.	GO:0004984;	GO:0004872;	GO:0007608;	InterPro; IPR004117; 7tm 6.	Pfam; PF02949; 7tm 6; 1.	Receptor.	SEQUENCE 447 AA; 51176 MW; 3AB7B4216F048BEB CRC64;	7 7 60	Similarity	rative 1
RESULT 1 Q963E7	ID 0963					GN GUR-										Ī		9 9	8	DR GO;	Inte		KW Recei	so seou	One TV Match	Best Loc	Matches

1 CVPLTC 6 |:|||| 302 CIPLTC 307 qq

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EQUENCE FROM N.A.

MEDLINE=21365705; PubMed=11472063;

MEDLINE=21365705; PubMed=11472063;

MEDLINE=21365705; PubMed=11472063;

Sun P.C., Uppaluri R., Scholnick S.B.;

Sunwoo J.B., Gollin S.M., Scholnick S.B.;

"Transcript map of the 8p23 putative tumor suppressor region.";

AT "Transcript map of the 8p23 putative tumor suppressor region.";

AT "Transcript map of the 8p23 putative tumor suppressor region.";

AT "Transcript map of the 8p23 putative tumor suppressor region.";

AT "Transcript map of the 8p23 putative tumor suppressor region.";

C = SIMILARITY: CONTAINS 14 CUB DOMAINS.

EMBL; AY017307; AAG52948.1; -

C = SIMILARITY: CONTAINS 1 -

C = SIMILARITY: SUPPRESSOR 1 -

C = SIMILARITY: SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ947L8.1.8 (Novel sushi (SCR repeat) domain protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.7%; Score 36; DB 4; Length 533;
83.3%; Pred. No. 17;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wallis J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AlJS5178; CAC10283.1; -.
HSSP; P10998; IVVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 AA; 57921 MW; 0554F7E10911F9BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             096QU9 PRELIMINARY; PRT; 3389 AA.
096QU9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CUB and subshi multiple domains protein 1 short form.
Homo sapiens (Human)
                                                                                                                                                                                                                              533 A.A.
Mismatches
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Pfam; PF00084; sushi; 8.
SMART; SM00032; CCP; 8.
                                                                                                                                                                                                                                 PRT;
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Matches 5; Conservative
Conservative
                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533
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                                                                                  |:[|||
125 CIPLTC 130
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                                                  1 CVPLTC 6
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SEQUENCE
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     Matches
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Pubmed=12908933,
Tovanabutra S., Watanaveeradej V., Viputtikul K., De Souza M.,
Razak M.H., Suriyanon V., Jittiwutikarn J., Sriplienchan S.,
Nitayaphan S., Benenson M.W., Sirisopana N., Remzullo P.O.,
Brown A.E., Robb M.L., Beyrer C., Celentano D.D., McNeil J.G.,
Brown A.E., Robb M.L., McUtchan F.E.,
M.New Circulating Recombinant Form, CRF15 01B, Reinforces the Linkage
Detween IDU and Heterosexual Epidemics in Thailand.";
AIDS Res. Hum. Retroviruses 19:561-567(2003).
EMBL, AF529572; AAQ09553.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.4%; Score 37; DB 5; Length 447; ilarity 83.3%; Pred. No. 9.2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                          Kershaw J.K.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Envelope protein.
SEQUENCE 849 AA; 96536 MW; D7AB6F8B670BAED3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02949; 7tm 6; 1. SEQUENCE 447 AA; 51227 MW; E916BEAA7C14C80C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WormPep; ZC504.5; CE30223.

GO; GO:00156020; C:membrane; IEA.

GO; GO:0005549; F:odorant binding; IEA.

GO; GO:0004984; F:olfactory receptor activity; IEA.

GO; GO:0007608; P:olfaction; IEA.
                                                                                                               Last sequence update)
Last annotation update)
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Pred. No. 16;
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                                       447 AA.
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                                                                                       Created)
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z50029; CAA90343.3; -.
PIR; T27621, T27621.
                                                                                    01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                          PRELIMINARY;
                                                                                                                                                                                                                      Caenorhabditis elegans.
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302 CIPLTC 307
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Best Local Similarity
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                                                                                                                                                                 ZC504.5 protein.
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Best Loc Matches

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94.78;
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les 5; Conservative
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184
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VARIANT
VARIANT
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Matches
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sun P.C., Uppaluri R., Schmidt A.P., Pashia M.E., Quant E.C., Sunwoo U.B., Gallin S.M., Scholnick S.B.;

Transcript map of the Bp23 putative tumor suppressor region.";

Genomics 75:17-25(2001).

-i - SINILARITY: CONTAINS 14 CUB DOMAINS.

EMBL, AYO17475; AG54083.1;

-MGD; MGI:2137383; CSMG1.
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Sun P.C., Uppaluri R., Schmidt A.P., Pashia M.E., Quant E.C.,
Sunwoo J.B., Gollin S.M., Scholnick S.B.;
"Transcript map of the 8p23 putative tumor suppressor region.";
Genomics 75:17-25 (2001).
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Pred. No. 88;
                                                                                                    4; Length 3389;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
PROSITE; PS00591; GLYCOSYL HYDROL F10; 1.
SEQUENCE 3389 AA; 370293 MW; 53C3009FCD3ED76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3564 AA; 387865 MW; 70824C55B0674609 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                              Score 36; DB 4
Pred. No. 84;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 3564 AA.
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Interpro; IPR000436; Sushi_SCR_CCP.
Ffam; PF00431; CUB; 14.
Ffam; PF00084; sushi; 28.
SMART; SM00032; CCP; 28.
SMART; SM0042; CUB; 14.
PROSITE; PS001180; CUB; 14.
SEQUENCE 3564 AA; 387865 MW; 7082
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MEDLINE=21365705; PubMed=11472063;
                                                                                              94.7%;
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Best Local Similarity 83.3'
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                             Query Match
Best Local Similarity
5; Conserv?
                                                                                                                                                                                                                                                                  2677 CVPITC 2682
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2923L3
AC 29223
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AC 201-D)
DT 01-D)
DT 01-D)
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296RM4
ID 096RM4
AC 096RM
DT 01-0)
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GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . ; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR0000595; CUB.

InterPro; IPR001000; Glyco_hydro_10.

InterPro; IPR001000; Glyco_hydro_10.

InterPro; IPR001001; Glyco_hydro_10.

Ffam; PF00431; CUB; 14.

PFam; PF00431; CUB; 14.

PRART; SM00042; CUB; 14.

PROSITE; PS00180; CUB; 14.

PROSITE; PS00191; GLYCOSYL HYDROL_F10; 1.

SEQUENCE 3566 AA; 388846 MW; 6126AB3013C4148C CRC64;
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EMBL; AF275336; AAG00977.1; --
EMBL; AL606722; CAR17596.1; --
EMBL; AL606722; CAR17596.1; --
EZFIN; ZDB-GENNE-980526-16; ednrbl.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IRR000776; GPCR_Rhodopsn.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
Endothelin receptor bl (SI:dZ27N24.3) (Endothelin receptor B)
[2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUN P.C., Uppaluri R., Schmidt A.P., Davis M.E., Quant E.C.,
Sun P.C., Gollin S.M., Scholnick S.B.,
Sunwoo J.B., Gollin S.M., Scholnick S.B.,
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 88;
1; Mismatches 0; Indels
                                                                                                                                                                                           SEQUENCE FROM N.A.

Tong B., Scholnick S.B.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS333704; AAK73475.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corby N.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00237; G PROTEIN RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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MEDLINE=21456161; PubMed=11572484;
Nagase T., Kikuno R., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XXI.
The complete sequences of 60 new cDNA clones from brain which code for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                 92.1%; Score 35; DB 11; Length 578; 83.3%; Pred. No. 30; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.1%; Score 35; DB 4; Length 946; 83.3%; Pred. No. 46; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 946 AA; 102543 MW; EDC903C6BD390B4A CRC64;
                                                                                                                                  578 AA; 64140 MW; C9F6DA810133FED7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein KIAA1884 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pregnancy-associated plasma protein-A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1367 AA
                                                                                                                                                                                                                                                                                                                                                                          946 AA
GO, GO:0030154, P:cell differentiation, InterPro; IPR000800; Notch dom. InterPro; IPR000436; Sushi_SCR_CCP. Pfam; PF000084; Sushi, 5. SWART; SM00032; CCP, 4. SMART; SM00004; NL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ES06;
01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      large proteins.";
DNA Res. 8:179-187 (2001).
EMBL, AB067471; BAB67777.1;
InterPro, IPR003006; Ig_MHC.
InterPro, IPR000456; Sughi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFam; PF00084; Bush; 12.
SMART; SM00032; CCP; 12.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                361 CVPVTC 366
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Matches 5; Conserv
                                                                                                                                                                                      Best Local Similarity
Matches 5; Conserv
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47 CVPVTC 52
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                                                                                                                                                                                                                                             1 CVPLTC 6
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                                                                                                                                  SEQUENCE
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Q9ES06
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Olesen C., Hansen C., Hayashizaki Y., Byskov A., Tommerup N.;
Olesen C., Hansen C., Hayashizaki Y., Byskov A., Tommerup N.;
Partial sequence of Mus musculus Mus musculus pregnancy-associated
plasma protein A (Pappa).";
Submitted (Apr.-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226433; AAF70319.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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01-07T-2003 (TrEMBLrel. 25, Last annotation update)
BM423P8.2 (Pregnancy-associated plasma protein A) (Fragment)
PAPPA.
                                                       92.1%; Score 35; DB 13; Length 426; 83.3%; Pred. No. 23; 0; Indels iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.1%; Score 35; DB 11; Length 468; 83.3%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn M.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL691454; CAD62274.1; -.
GO; GO:0016020; C:membrane; IEA.
     318 318 W -> *.
426 AA; 48770 MW; F92COBD3046E4A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468 AA; 51134 MW; 85768E10D7D34FDA CRC64;
                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
Pregnancy-associated plasma protein A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:97479; Pappa.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0030154; P:Cell differentiation; IEA.

InterPro; IPR000800; Notch dom.

InterPro; IPR000436; Sushi_SCR_CCP.

Pfam; PR00084; sushi; S.

SMART; SM00032; CCP; 4.
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01-0TN-2003 (TrEMBLrel. 24, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                PRT;
                                                                          Local Similarity 83.3
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                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                      265 CMPLTC 270
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SEQUENCE
     VARIANT
SEQUENCE
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REPRESENTATIONS OF SOLUTIONS OF

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"Expression of recombinant murine PAPP-A and a novel variant (PAPP-Ai) with differential proteolytic activity.";
With differential proteolytic activity.";
EMBL. J. Blochem. 0:0-0(2002).
EMBL; AF439514; AAM12688.1; -.
MGD; MGI:97479; Pappa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Soe R., Overgaard M.T., Thomsen A.R., Laursen L.S., Olsen I.M., Haaning J., Sottrup-Jensen L., Haaning J., Giudice L.C., Conover C.A., Oxvig C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                          DB 11; Length 1545; 70;
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   Pfam; PF00084; sushi; 5.
SMART; SM00032; CCP; 4.
SMART; SM00066; LamGL; 1.
SMART; SM00004; NL; 3.
PROSITE; PS00112; ZINC_PROTEASE; 1.
NON_TER 1 1 1.
SEQUENCE 1545 AA; 172584 MW; B820BF9998245419 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0UN-2002 (TrEMBLrel. 21, Created)
01-0UN-2002 (TrEMBLrel. 21, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Pregnancy-associated plasma protein-A variant (Fragment).
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R GO; GO:001620; C:nembrane, IEA.

GO; GO:000827; F:netallopeptidase activity; IEA.

GO; GO:0008270; F:netallopeptidase activity; IEA.

R GO; GO:0008270; F:netallopeptidase activity; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR006898; Comal like lec_gl.

R InterPro; IPR006809; Lang like.

R InterPro; IPR006558; Lang like.

R InterPro; IPR006559; Lang like.

R InterPro; IPR006051; Peptidase M43B.

R InterPro; IPR0060436; Sushī SCR CCP.

R Ffam; PP05572; Peptidase M46; I.

R Ffam; PP0031; CCP; 4.

SMART; SW0056; Langli, 1.
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                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                          Score 35;
Pred. No. 7
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PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                    Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               1328 CVPVTC 1333
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SEQUENCE
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Q7Z408;
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Q8R4K7
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AC Q7
            SO FIT SO S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                               EMBL, AF258461; AAG09799.1; -.

EMBL, AF258461; AAG09799.1; -.

R MEROPS; McG.001; -.

MGD, MGI.97479; Pappa.

GO; GO:0016270; F:metallopeptidase activity; IEA.

GO; GO:0008270; F:metallopeptidase activity; IEA.

GO; GO:0008270; F:metallopeptidase activity; IEA.

GO; GO:000154; P:cell differentiation; IEA.

R GO; GO:000508; P:proteolysis and peptidolysis; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R InterPro; IPR000805; Notch dom.

R InterPro; IPR000805; Pept M Zn BS.

InterPro; IPR000815; Pept M Zn BS.

InterPro; IPR000815; Sushī ĞCR_CCP.

Pfam; PF00084; Sushī, 5.

R SMART; SM00032; CCP; 4.

SMART; SM00032; CCP; 4.

SMART; SM00004; NL; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Pregnancy-associated plasma protein-A (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 83.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1150 CVPVTC 1155
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CVPLTC 6
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                                 STRAIN=C57BL/6J;
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CUB and sushi multiple domains 2.

OS Homo sapiens (Human)
OC BUKATYOCA; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI.TaxID=9606;
RN MEDLINE-22788796; PubMed=12906867;
RN MEDLINE-22788796; PubMed=12906867;
RX MEDLINE-2288 CAVPTC 2593

Query Match
SEQUENCE 3487 AA; 380035 MW; 3A77D8457DF8EFB5 CRC64;
Authority Match
SEQUENCE 3487 AA; 380035 MW; 3A77D8457DF8EFB5 CRC64;
Ouery Match
SEQUENCE 3487 AA; 380035 MW; 3A77D8457DF8EFB5 CRC64;

Query Match
SEQUENCE 5; Conservative 1; Mismatches 0; Indels 0; Gaps
OY 1 CVPLTC 6

DD 2588 CVPVTC 2593

Search completed: September 5, 2004, 10:00:05
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Compugen Ltd.
GenCore version (c) 1993 - 2004
                                                - protein search, using sw model
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5, 2004, 09:37:49 ; Search time 19.697 Seconds (without alignments) 86.068 Million cell updates/sec September Run on:

US-09-761-636A-12 38 Perfect score: Title:

1 CVPLTC 6 **BLOSUM62** Scoring table: Sequence:

1586107 seqs, 282547505 residues Searched:

Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seg DB Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A\_Geneseq\_29Jan04:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp1980s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. AAU04531 standard; peptide; 6 AA. VEGF based monocyclic peptide 9. (first entry) 26-SEP-2001 AAU04531; AAU04531 ID AAU 

Synthetic.

Location/Qualifiers 1. .6 /note= "This bond cyclises the peptide" 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533. Key Disulfide-bond WO200152875-A1. 26-JUL-2001.

(LUDW-) LUDWIG INST CANCER RES.

Stacker S, Hughes RA, Achen MG,

Cendron A;

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine WPI; 2001-442248/47.

Claim 49; Page 32; 102pp; English.

residues.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis.

To cyclisation are used to interfere with anglogenesis.

To cyclisation or lymphanglogenesis in a mammal with a condition characterised by anglogenesis, neovascularisation or lymphanglogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy.

The condition is diabetic retinopathy, psoriasis, arthropathy.

Cerebrovascular accident, post-angloplasty restenosis, head, heat or cramma, substance-induced neovascularisation of the liver, excessive trauma, substance-induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular or sequelae, hypertension induced neovascular or sequelae, hypertension induced neovascular or sequelae, hypertension induced neovascular continued neovascular continued neovascular continual has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic or brain. The peptides are used to image blood vessels and lymphatic with at least one biological activity induced by WEGF. VEGF-C or -D and chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORFX; human; pharmacogenomics; cancer; hyperproliferative disorder; dysproliferative disorder; neurodegenerative disorder; organ transplant; cardiovascular disease; cytokine; cell proliferation; immunomodulatory; cell differentiation; haematopoiesis; tissue growth; thrombolytic; nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; cytostatic; antidiabetic; virucide; antiinfertility; anticonvulsant; assortopic; antidiabetic; virucide; antiinfertility; anticonvulsant; ansortopic; antidiabetic; transplantiation; carebroprotective; hepatotropic; antiinflammatory; tumour inhibition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6;
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100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mishnu VS,
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05-APR-2001; 2001US-00826734.
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Zerhusen BD, Kekuda R;
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N-PSDB; ABA90195.
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Matches 6; Conserv
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New polypeptides and polynucleotides, useful for treating diseases such as cancer, Alzheimer's disease, atherosclerosis, diseases associated with liver, comprises polypeptides and polynucleotides of open reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Immunoglobulin superfamily protein; IgSF; Immune response; inflammatory response; cell-cell interaction; cell-surface recognition; neural disorder; immune system disorder; muscular disorder; cardiovascular disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; proliferative disorder; common variable adhesion deficiency syndrome; AIDS; SCID; acquired immunodeficiency syndrome; anaemia; rheumatoid arthritis; Alzheimer; a disease; Crohn's disease; liver cancer; leukaemia; Hodgkin's lymphoma; Parkinson's disease; Huntingdon's disease; dementia; artherosclerosis; stroke; diabetes mellitus; Addison's disease; urticaria; severe combined immunodeficiency; antibody.
                                                                                                                                                                                                   The present invention provides the protein and coding sequences of human OREX, where X is any number between 1 and 132. These sequences can be used to diagnose and treat OREX related disorders, including cancer, hyperproliferative and dysproliferative disorders, including cancer, insorders, disorders related to organ transplantation or cardiovascular diseases, and may have cell proliferation or differentiation, cyrokine, immunomodulatory, haematopoiesis regulating, tissue growth, inhibin or activin, chemotactic or chemokinetic, haemostatic or thrombolytic and/or antinflammatory activities. The present sequence is one of the OREX
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/label= Immunoglobulin_like_domain
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/label= Immunogenic_epitope
328. .336
/label= Immunogenic_epitope
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|label=_Immunogenic_epitope
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/label= Immunogenic_epitope
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/label= Immunogenic_epitope
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                                                                                                                                                        Claim 11; Page 82; 111pp; English.
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/label= Imm.
392. .4
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Region

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Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
        184. .500
/label= Immunogenic_epitope
/label= Immunogenic_epitope
                            /label= Immunogenic_epitope
                                   577. .583
/label= Immunogenic_epitope
                                                        /label= Immunogenic_epitope
                                                                                                                                                                                                        Claim 11; Page 238-239; 247pp; English.
                                                                                                                                                                                    Isolated nucleic acid molecule
                                                                                                 29-AUG-2000; 2000WO-US023662.
                                                                                                               99US-0152248P.
                                                                                                                            (HUMA-) HUMAN GENOME SCI INC. (NIJJ/) NI J.
                                                  .610
                      517
                                                                                                                                                  Ruben SM,
                                                                                                                                                                WPI; 2001-203084/20.
                                                                                                                                                                       N-PSDB; AAS00146.
                                                                       WO200118176-A1.
                                                                                                               03-SEP-1999;
                                                                                   15-MAR-2001
                                                                                                                                                  Young PE,
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The sequence is a Human Immunoglobulin superfamily, IgSF, protein, a diverse family of proteins involved in cell-cell interactions, cell-cautherse family of proteins involved in cell-cell interactions, cell-cauther sequence in the companies. Companies of surface to the present invention are useful to provide immunological polypeptides of the present invention are useful to provide immunological probes for differential identification of tissues. Antibodies can be used to assay levels of polypeptides encoded by polynucleotides of the invention. Polypeptides of the present invention can be used to treat or prevent diseases or conditions such as neural disorders, immune system disorders, pulmonary disorders, reproductive disorders, and/or cancerous diseases and disorders, proliferative disorders, and/or cancerous diseases and conditions. Polynucleotides of the invention are also useful in treating the above disorders. Examples of the disorders include common variable adhesion deficiency syndrome, acquired immunodeficiency syndrome (AIDS), conduitions, relevance in the invention are also useful in treating anemia, rheumatoid arthritis, Alzheimer's disease, Crohn's disease, Cliver cancer, leukaemia, Hodgin's lymphoma, parkinson's disease, dementia, artherosclerosis, stroke, diabetes conduition, and assay and an emiliar, and are seamples of diseases and disorders are given in the continuation.
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Matches
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94.7%; Score 36; DB 4; Length 613; 83.3%; Pred. No. 6.7e+02; ive 1; Mismatches 0; Indels
                                  5; Conservative
                                                               1 CVPLTC 6
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AAB83372 standard; protein; 882 AA. |||:|| 264 CVPITC 269 RESULT

NOV16 protein sequence.

26-MAR-2002 (first entry) AAB83372; AABB3372 ID AABB XX AC AABB XX DT 26-M XX DB NOV1

NOV, Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase. Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome; cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome; therapy; NOV1; NOV2; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10;

Unidentified.

WO200136638-A2.

25-MAY-2001

17-NOV-2000; 2000WO-US031543

19-NOV-1999; 99US-0166336P. 29-NOV-1999; 99US-0167785P. 08-MAR-2000; 2000US-0187844P. 19-NOV-1999;

16-NOV-2000; 2000US-00715417 

(CURA-) CURAGEN CORP.

Щ ., Fernandes Vernet C, Shimkets RA, Lichenstein H,

WPI; 2001-648134/74. N-PSDB; AAF87127. Novel human polypeptides and the nucleic acids that encode them useful for preventing, diagnosing and treating e.g. cancer, inflammation and for preventing, di immune disorders.

Claim 1; Page 50-52; 141pp; English.

NOV16 proteins, and their coding sequences. The proteins have Cytostatic; contraceptive; antiinflammatory; immunomodulatory; and cardiovascular (e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception) MOV2-3, NOV6 and NOV9 are homologous to the epidermal growth factor (EGP) like Super family and are involved in, e.g. regulation of cell development, apoptosis, cell addresion, growth migration, cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders. serine/threonine kinases, and are used to treat kinase-related disorders This sequence is the NOV16 protein. The invention relates to the NOV1-NOV6-10 are homologous to EGF-like fibrillin proteins and are used to treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-QT syndrome and marfan syndrome

Sequence 882 AA;

Gaps . 0 94.7%; Score 36; DB 4; Length 882; 83.3%; Pred. No. 9.2e+02; ive 1; Mismatches 0; Indels 5; Conservative Best Local Similarity Matches 5; Conserva Query Match

0;

(e.g. Peutz-Jeghers syndrome, cellular proliferation and contraception). NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (BGF) NOV2-3, NOV6 and NOV8 are homologous to the epidermal growth factor (BGF) development, apoptosie, cell adhesion, growth migration, cell structure and motility and protein management, and are used to treat cancers, inflammatory disorders, immune disorders and cellular adhesion disorders. NOV6-10 are homologous to BGF-like fibrillin proteins and are used to treat cardiovascular disease e.g. hypertrophic cardiomyopathy, long-OT

syndrome and marfan syndrome

888888888888888

Sequence 883 AA;

Peutz-Jeghers syndrome, cellular proliferation and contraception)

0

Gaps ..

Length 883; 0; Indels

Score 36; DB 4; 1 Pred. No. 9.2e+02; 1; Mismatches 0;

83.3%;

Query Match Best Local Similarity 83...

264 CVPITC 269

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1 CVPLTC 6

8 8

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NOV; Cytostatic; contraceptive; antiinflammatory; immunomodulatory; cardiovascular; casein kinase II phosphorylation site; contraception; serine/threonine kinase; Peutz-Jeghers syndrome; cellular proliferation; epidermal growth factor; cell development; apoptosis; cell adhesion; growth migration; cell structure; motility; cancer; immune disorder; inflammatory disorder; cellular adhesion disorder; long-QT syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiovascular disease; hypertrophic cardiomyopathy; marfan syndrome;
therapy; NOV1; NOV2; NOV3; NOV4; NOV5; NOV6; NOV7; NOV8; NOV9; NOV10;
NOV11; NOV12; NOV13; NOV14; NOV15; NOV16.
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                                                                                                                                                                                                                      AAB83371 standard; protein; 883 AA.
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29-NOV-1999; 99US-0167785P.
08-MAR-2000; 2000US-0187844P.
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                                                        264 CVPITC 269
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CVPLTC 6
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                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
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Human C3b/C4b complement receptor like protein #1.

(first entry)

01-JUL-2002

AAE20787;

AAE20787 standard; protein; 3069 AA.

RESULT 6 AAE20787

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Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid arthritis, psioriatic arthritis, inflammatory arthritis, and multiple
                                                                      Human, C3b/C4b complement receptor-like molecule; immune system disorder; gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory arthritis; inflammatory joint disease; Alzheimer's disease; untilple sclerosis; inflammatory powel disease; nervous system disorder; transplant rejection; autoimmune disease; ischaemic condition; motropic; metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus; infertility; vasodilator; obesity; cardiant.
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                   label= Unknown
                                                                                                                                                                                                                                                                                                               /label= Unknown
                                                                                                                                                                                                                                                              label= Unknown
                                                                                                                                                                                                                                                                                        label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                               24-JUL-2001; 2001WO-US023232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-303934/34.
                                                                                                                                                                                                                                                                             Misc-difference 586
                                                                                                                                                                                                                                                   Misc-difference 461
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                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sclerosis.
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This sequence is the NOV15 protein. The invention relates to the NOV1NOV16 proteins, and their coding sequences. The proteins have Cytostatic;
Contraceptive; antiinflammatory; immunodulatory; and cardiovascular
activities. The sequences may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate NOVX expression. They
crecifying mutations or deletions in a patient's genome that affect the
activity of protein by expressing inactive proteins or to supplement the
patients own production of protein. They are used to produce NOVX
proteins, by inserting the nucleic acid into a cell and culturing it to
express the protein. The DNA may be used as DNA probes in assays to
detect and quantitate the presence of similar DNAs in samples, and which
cas antigens in the production of antibodies (Abs) against NOVX and in
cas antigens in the production of antibodies (Abs) against NOVX and in
assays to identify modulators of NOVX expression and activity. The anti-

NOVX Abs and antegonist are used to down regulate expression and activity. The anti-NoVX Abs are used for detecting the presence of NOVX in samples. Disorders that may be prevented, diagnosed and/or treated vary depending on the NOVX protein. NOV1, NOV3, NOV7, NOV9-11 and NOV13-16 have casein kinase II phosphorylation sites characteristic of serine/threonine kinases, and are used to treat kinase-related disorders

Claim 13; Fig 1; 251pp; English

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The invention relates to a nucleic acid encoding a novel C3b/C4b complement receptor (CR) like nucleic acid molecule. The C3b/C4b CR-like polypeptide and nucleic acid molecules may be used to treat, prevent, ameliorate, diagnose and/or detect diseases such as immune system disorders such as rheumatoid arthritis, pillammatory joint disease, autoimmune arthritis, inflammatory joint disease, autoimmune arthritis, inflammatory boint disease, unlippe sclerosis, lupus, inflammatory bowel disease, transplant rejection, nervous system disorders (e.g. Alzheimer's disease), ischaemic conditions, metabolic disorders (e.g. obssity and disease) and infertility. The invention is useful in gene therapy. The present sequence is human C3b/C4b complement receptor like protein. Note: The present sequence is stated to be the same as that referred to as SEQ the sequences differ at position 695 the specification. However
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Pred. No. 2.8e+03;
1; Mismatches 0; Indels
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Best Local Similarity 83.3%,
Local S; Conservative
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The invention relates to a nucleic acid encoding a novel C3b/C4b complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like Dolypeptide and nucleic acid molecules may be used to treat, prevent, ameliorate, diagnose and/or detect diseases such as immune system disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, psoriatic arthritis, inflammatory disease, autoimmune conferes, lupus, inflammatory bowel disease, cransplant rejection, nervous system disorders (e.g. Alzheimer's disease) ischaemic conditions, metabolic disorders (e.g. Alzheimer's chabetes) and infertility. The invention is useful in gene therapy. The present sequence is human C3b/C4b complement receptor like protein, alternative version. Note: The present sequence is stated to be the same cas that referred to as SEQ ID NO:2 (AABE20787) shown in figure 1 of the specification. However the sequences differ at position 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                               Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid arthritis, psioriatic arthritis, inflammatory arthritis, and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy, rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory athritis; inflammatory joint disease; Alzheimer's disease; multiple sclerosis; inflammatory bowel disease; nervous system disorder; transplant rejection; autoimmund disease; ischaemic condition; nootropic; metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus; infertility; vasodilator; obesity; cardiant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; C3b/C4b complement receptor-like molecule; immune system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 5; Length 306
Pred. No. 2.8e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Xaa can be any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat C3b/C4b complement receptor like protein.
                                                                                                                                    Claim 13; Page 176-189; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE20788 standard; protein; 3095 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Unknown
/note= "Xaa can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ۲,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2000; 2000US-0222504P.
28-NOV-2000; 2000US-00728787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
WPI; 2002-303934/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CVPITC 2243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CVPLTC 6
                N-PSDB; AAD33318.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3069 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200210199-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
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                                                                                                     sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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The invention relates to a nucleic acid encoding a novel C3b/C4b complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like polypeptide and nucleic acid molecules may be used to treat, prevent, ameniorate, diagnose and/or detect diseases such as immune system disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory arthritis, osteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lugus, inflammatory bowel disease, transplant rejection, nervous system disorders (e.g. Alzheimer's disease), ischaemic conditions, metabolic disorders (e.g. obesity and diabetes) and infertility. The invention is useful in gene therapy. The present sequence is rat C3b/C4b complement receptor like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, C3b/C4b complement receptor-like molecule; immune system disorder; gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory arthritis; inflammatory joint disease; Alzheimer's disease; multiple sclerosis; inflammatory bowel disease; nervous system disease; transplant rejection; autoimmune disease; ischaemic condition; nootropic; metabolic disorder; immunomodularory; neuroprotective; diabetes; lupus; infertility; vasodilator; obesity; cardiant.
                                                                                                           Nucleic acid encoding a novel C1b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid arthritis, psioriatic arthritis, inflammatory arthritis, and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 5; Length 309
Pred. No. 2.8e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human C3b/C4b complement receptor like protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE20789 standard; protein; 3100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Unknown
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                                                                                                                                                                                                   Claim 13; Fig 3; 251pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2001; 2001WO-US023232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                               Welcher AA, Elliott GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2264 CVPITC 2269
                                                                 2002-303934/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CVPLTC 6
AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3095 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                    N-PSDB; AAD33319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2002
                                                                                                                                                                      sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE20789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
(AMGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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The invention relates to a nucleic acid encoding a novel C3b/C4b complement receptor (CR)-like nucleic acid molecule. The C3b/C4b CR-like polypeptide and nucleic acid molecules may be used to treat, prevent, ameliorate, diagnose and/or detect diseases such as immune system disorders such as rheumatorid arthritis, psoriatic arthritis, inflammatory arthritis, posteoarthritis, inflammatory joint disease, autoimmune disease, multiple sclerosis, lupus, inflammatory bowel disease, disease, multiple sclerosis, lupus, inflammatory bowel disease, disease), ischaemic conditions, metabolic disorders (e.g. Alzheimer's disease), ischaemic conditions, metabolic disorders (e.g. obesity and diabetes) and infertility. The invention is useful in gene therapy. The present sequence is stated to be the same as that referred to as SEQ ID NO:7 (AAE20901) shown in page 239-251 of the specification. However the sequences differ at position 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, C3b/C4b complement receptor-like molecule; immune system disorder; gene therapy; rheumatoid arthritis; psoriatic arthritis; osteoarthritis; inflammatory arthritis; inflammatory joint disease; Alzheimer's disease; multiple solerosis; inflammatory bowel disease; nervous system disorder; transplant rejection; autoimmune disease; ischaemic condition; nootropic; metabolic disorder; immunomodulatory; neuroprotective; diabetes; lupus; infertility; vasodilator; obesity; cardiant.
                                                                                                                                                                   Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid arthritis, psioriatic arthritis, inflammatory arthritis, and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human C3b/C4b complement receptor like protein #2, alternative version.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 5; Length 3100;
Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE20901 standard; protein; 3100 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Unknown
/note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= Unknown
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                                                                                                                                                                                                                                                               claim 13; Fig 2; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.7%;
83.3%;
2000US-0222504P.
2000US-00728787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2269 CVPITC 2274
                                                                                        Elliott
                                                                                                                           WPI; 2002-303934/34.
N-PSDB; AAD33320.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3100 AA;
                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-2002
   02-AUG-2000;
28-NOV-2000;
                                                                                          Welcher AA,
                                                                                                                                                                                                                                  sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE20901;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Gaps

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The invention relates to a nucleic acid encoding a novel C3b/C4b

Complement receptor (CR)-like nucleic acid molecule. The G3b/C4b CR-like

Dolypoptide and nucleic acid molecules may be used to treat, prevent,

ameliorate, diagnose and/or detect diseases such as immune system

disorders such as rheumatoid arthritis, psoriatic arthritis, inflammatory

arthritis, osteoarthritis, inflammatory joint disease, autoimmune

clasease, multiple solerosis, lupus, inflammatory bowel disease,

transplant rejection, nervous system disorders (e.g. Alzheimer's

clasease), ischaemic conditions, metabolic disorders (e.g. Alzheimer's

disease), ischaemic conditions, metabolic disorders (e.g. Abcheimer's

clabetes, and infertility. The invention is useful in gene therapy. The

present sequence is human C3b/C4b complement receptor like protein,

alternative version. Note: The present sequence is stated to be the same

cc as that referred to as SEQ ID NO:7 (AAE20789) shown in figure 2 of the

specification. However the sequences differ at position 726
                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding a novel C3b/C4b Complement Receptor-like nucleic acid molecule, useful for treating, preventing and diagnosing rheumatoid acid missing psioriatic arthritis, inflammatory arthritis, and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 239-251; 251pp; English.
                                                                                                                                               02-AUG-2000; 2000US-0222504P.
28-NOV-2000; 2000US-00728787.
                                                                                                       24-JUL-2001; 2001WO-US023232.
                                                                                                                                                                                                                                                       Elliott GS;
                                                                                                                                                                                                                                                                                                 2002-303934/34.
                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3100 AA;
                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD33320
                      WO200210199-A2
                                                                                                                                                                                                                                                     Welcher AA,
                                                                07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                             sclerosis.
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94.7%; Score 36; DB 5; Length 3100; 83.3%; Pred. No. 2.8e+03; 0; Indels 1; Mismatches 5; Conservative Local Similarity Query Match Matches

|||:|| | 2269 CVPITC 2274 1 CVPLTC 6 à

ABG79168 standard; protein; 3104 AA. ABG79168; RESULT 11 ABG79168 MARKA KARAKA KAR

(first entry) 15-NOV-2002

Human cub and sushi domain containing protein #1.

Parkinson's disease; Huntington's disease; neurological disorder; schizophrenia; manic depression; mental retardation; angina pectoris; cardiovascular disease; acute heart failure; mycocardial infarction; muscular disease; muscular disorder; retinal disease; photoreception; definences; keratinisation disorder; retinal disease; photoreception; immunological disorder; inflammatory disease; immune disease; diabetes; bacterial infection; fungal infection; protozoal infection; obesity; viral infection; reproductive system disorder; metabolic disturbance; anorexia, wasting disorder; chronic disease; infectious disease; dyslipidaemia; cub; sushi; myelin; von willebrand factor; kielin; semaphorin; serine/threonine protein kinase; TGF-beta binding; mas proto-oncogene; ribonuclease pancreatic precursor; aminotransferase; Human; NOVX; neurodegenerative disease; Alzheimer's disease; anxiety;

as a result of a single by Gly as a result of a single (SNP)" as a result of a single tolloid-like 2; cysteine sulfinic acid decarboxylase SNP; by Thr (SNP)" by Ala (SNP)" /note= "Asp substituted nucleotide polymorphism /note= "Ala substituted nucleotide polymorphism /note= "Val substituted nucleotide polymorphism Location/Qualifiers 1027 single nucleotide polymorphism. 08-DEC-2000; 2000US-02564329P. 14-DEC-2000; 2000US-025648P. 15-MAY-2001; 2001US-0291037P. 08-UUN-2001; 2001US-0297173P. 08-UUN-2001; 2001US-0309258P. 29-AUG-2001; 2001US-0315639P. 10-DEC-2001; 2001WO-US048369 2001US-0326393P misc difference 1084 misc\_difference 1362 misc difference WO200264791-A2. Homo sapiens 01-OCT-2001; 22-AUG-2002 

(CURA-) CURAGEN CORP.

Alsobrook JP, Anderson DW, Burgess CE, Boldog FL, Casman SJ; Colman SD, Edinger SR, Bllerman K, Gerlach V, Gorman L, Grosse WM; Guo K, Herrmann JL, Kekuda R, Lepley DM, Li L, Macdougall JR; Millet I, Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shimkets RA; Smithson G, Spytek KA, Stone DJ, Tchernev VT, Vernet CAM, Voss EZ; Zhong M; Spytek KA, Zhong H, Z Smithson G, { Zerhusen BD,

WPI; 2002-643486/69. N-PSDB; ABS64375 New NOVX polypeptides and polynucleotides useful for treating or preventing e.g. neurodegenerative diseases, neurological disorders, cardiovascular diseases, muscular diseases and disorders, or immunological diseases.

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Gaps

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Claim 1; Page 13-14; 299pp; English.

The present invention relates to new NOVX polypeptides. The polypeptides, polymucleotides and antibodies are useful in the manufacture of a medicament for treating or preventing neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease, or Huntington's disease; (e.g. Alzheimer's disease).

Alzheimer's disease, Parkinson's disease (e.g. acute heart failure, comencal retardation), cardiovascular disease (e.g. acute heart failure, compania pectoris or myocadial infarction), muscular diseases and diseases including those involving photoreception, definess and keratinisation disorders), cancer (e.g. ovarian cancer or melanoma), immunological disorders, inflammatory and immune diseases, bacterial, fungal, protozal and viral infections, and reproductive or expression, cardios or compounds that modulate the NOVX protein activity or expression, as well as to treat disorders characterised by insufficient or excessive production of NOVX protein forms that have decreased or aberrant activity compared to NOVX wild type protein, such as diabetes, obesity, metabolic disturbances associated with chronic diseases and various cancers, infections diseases and various dyslipidaemias. The nucleic acid sequences of the invention may be used in chromosome mapping, identifying an individual from minute biological samples (tissue typing), and in forensic identification of a biological sample. The present amino acid sequence represents a NOVX protein of the invention Sequence 95 AA;

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by 2. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervolved in binding apprenties. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies of precipit for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and characterianing P. acnes presence, for example, by diagnostic agents for determining P. acnes presence, for example, by contained in electronic format directly from WIPO at this patent did not form part of the printed specification, but was of the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris.
                                                                 .
0
                             Score 36; DB 5; Length 3104;
Pred. No. 2.8e+03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bhatia A;
                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes immunogenic protein #9095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitcham JL, Wang S
Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 9394; 1069pp; English.
                                                                                                                                                                                                                             AAU48199 standard; protein; 95 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Persing DH, M
                                                                                                                                                                                                                                                                                                 27-FEB-2002 (first entry)
                Query Match
Best Local Similarity 83...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes.
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N-PSDB; AAS59542.
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2486 CVPITC 2491
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                                                                                                        1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           maisonneuve J,
Sequence 3104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-2001
                                                                                                                                                                                                                                                                AAU48199;
                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                AAU48199
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for

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conciding a Propionibacterium acnes protein. The invention also relates to encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention and to additionally encompasses expression vectors and host cells comprising a dadditionally encompasses expression vectors and host cells comprising a polymucleotide of the invention, a immune response specific for a P. acnes polypeptide and an isolated T cell bopulation comprising T cells prepared to polypeptide and an isolated T cell bopulation comprising P. acnes polypeptides, via this method; a vaccine composition (comprising P. acnes polypeptides, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient, and a method for inhibiting the development of P. acnes in a patient, and a method for inhibiting the development of P. acnes in compression, or continuous or antigen-presenting cells that express the polypeptides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the colypeptides are useful for diagnosing, preventing or treating acnes of protein. The populations or antigen-presenting cells that express the colypeptides are useful for diagnosing, preventing or treating acnes or protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the estimate and the kit is useful for performing a diagnostic assay. The present canding frame) contained within the P. acnes polymucleotides of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maisonneuve JL;
Jones R, Carter D;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes predicted ORF-encoded polypeptide #9394.
                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                               vulgaris; antiseborrhoeic; dermatological; antibacterial;
                   Length 95;
                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bhatia A,
Benson DR,
                   Score 35; DB 4; I
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 9394; 1481pp; English.
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                     ABM44718 standard; protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-2001; 2001US-00978825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2002; 2002WO-US032727.
                     92.1%;
83.3%;
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                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes.
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Query Match
Best Local Similarity
Local 5; Conserve
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CVPVTC 67
                                                                                                        1 CVPLTC 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003033515-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-APR-2003
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                                                                                                                                                                                                                                                                                              ABM44718;
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Human adipocyte Selected Interacting Domain (SID) prey protein #1173.

(first entry)

15-JAN-2004

ADD27716;

ADD27716 standard; protein; 368 AA.

Adipocyte; protein-protein interaction; protein complex; bait-prey complex; Selected Interacting Domain; SID; drug; drug discovery; metabolic disease; obseity; lipodystrophy; diabetes mellitus; type 2; non-insulin dependent; NIDDM; adipogenesis modulation; gene therapy; human.

Sun

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invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at frp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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                                                                                        Score 35; DB 6; Length 95;
Pred. No. 1.8e+02;
1; Mismatches 0; Indels
                                                                             92.1%; Sco...
83.3%; Pred. No. 1...
1; Mismatches
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                                                                                                                                                                                                                                                    ADA55489 standard; protein; 310 AA.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
                                                                                                                                                                                                                                                                                                                                           Human protein, SEQ ID 3057.
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                       Query Match
Best Local Similarity 83.37
S; Conservative
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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                                                                                                                                                                            62 CVPVTC 67
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                                                                                                                                               1 CVPLTC
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                                                           Sequence 95
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                                                                                                                                                                                                                                                                                 ADA55489;
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                                                                                                                                                                                                                                       ADA55489
 S S S S X S
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New complex of bait and prey between two polypeptides or polynucleotides encoding the two polypeptides of adipocytes, useful for selecting a modulating compound that inhibits or activates protein-protein

Claim 6; SEQ ID NO 1173; 232pp; English.

interactions

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rno

Khrebtukova I,

Мао Ј,

Whiteside S,

Legrain P,

WPI; 2003-111975/10.

N-PSDB; ADD27715

(HYBR-) HYBRIGENICS. (LYNX-) LYNX THERAPEUTICS INC.

03-MAY-2002; 2002WO-EP006333. 04-MAY-2001; 2001US-028885P.

WO200290544-A2.

14-NOV-2002,

Homo sapiens.

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The invention relates to a bait-prey complex between two adipocyte polypeptides, or between two polynucleotides encoding adipocyte polypeptides. The invention also relates to Selected Interacting Domain (SID) polypeptides which interact with selected bait polypeptides; polynucleotides encoding SID polypeptides; vectors comprising SID polynucleotides recombinant host cells comprising an adipocyte polynucleotide or a SID-encoding vector; a method of selecting for a compound which modulates interactions between adipocyte polypeptides; pharmaceutical composition comprising an adipocyte modulator, or a SID-encoding vector or host cell; and a protein chip comprising adipocyte bait polypeptides. The bait-prey complexes of the invention are useful interactions between adipocyte polypeptides. The material composition that inhibits or activates protein protein contractions between adipocyte polypeptides. The modulatory compounds identified can be used in the treatment of metabolic diseases such as obesity, lipodystrophy and type 2 diabetes mellitus, and in the condulation of adipocyte SID prey polypeptide of the invention.
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83.3%; Pred
1;
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Gaps

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Length 310;

Score 35; DB 6; Length siv. Pred. No. 5.3e+02;

92.1%; Scor. 83.3%; Pred. No. 5... 1; Mismatches

5; Conservative

Local Similarity

Query Match

Sequence 310 AA;

CLPLTC 267

262

1 CVPLTC 6

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5, 2004, 10:00:15; Search time 16.8485 Seconds (without alignments) 112.199 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/RCT_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1298764 seqs, 315065143 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
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38
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Segretice 12, Appl	Semience 184333,	Semiona o han!	Segmence 3, Appli	Segmence 2, Appli	Semione 17, Appl	Sequence 2206, Ap	Sequence 46, Appl	Sequence 45, Appl	Sequence 198429,	Sequence 3057, Ap	Sequence 25, Appl	Sequence 663, App	Sequence 272858,	seduence 3842, Ap
SUMMARIES	QI.	US-09-761-636A-12	US-10-424-599-164353	US-09-826-734-122	US-09-799-514-9	US-10-016-248-2	US-10-016-248-47	US-10-408-765A-2286	US-10-016-248-46	IIS-10-016-248-45	115-10-424-599-198420	US-10-094-749-3057	IIS-09-983-025-25	118-10-295-023	TIS-10-424-E00-2220E0	US-10-104-047-3843	7500 (50 101 01 02
		σ	12	12	6	12	12	16	12	12		15		, <u>c</u>	12	12	
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* Query	Match	100.0	100.0	94.7	94.7	94.7	94.7	94.7	94.7	94,7	92.1	92.1	92.1	92.1	89.5	89.5	
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16	33		52	16	US-10-437-963-19024	2
17	33		58	12	US-10-424-599-25235	25235
18	33	86.8	9	12	US-10-424-599-1984	1984
19	33		62	12	US-10-424-599-17080	equence 17080
20	33		69	12	US-10-424-599-14531	Panience 14531
21	33		103	12	US-10-424-599-21771	POLICE
22	33		149	12	US-10-425-114-60690	Semience 60690 A
23	33		158	12	US-10-282-122A-445	Semience 44515 A
24	33		162	12	US-10-425-114-50640	Semience 50640 A
25	33		187	12	US-10-425-114-50780	Segmence 50340, A
56	33		556	σ	US-09-815-923-6	Segmence 6 appli
27	33			12	US-10-262-83	Segmence 212 Appril
28	33		1587	σ	US-09-845-583-10	Semience 10 Appl
29	33			12	US-10-262-839-21	
30	32		34	16	US-10-437-963-200127	Semience 210, App
31	32		49			Sections 83 Anni
32	32		49		US-09-904-615-83	Segmence 83 Appl
33	32		49	14		Semience 92, Appl.
34	32		49	4		Semience 83 Appl
35	32		55	N	20724	Semience 33, Appl
36	32		57	N	24092	Semience 20/242,
3.7	32		117	N		man ha
38	32		125		1000	
39	3.2		164	c	6/99#-TG/-#00	drenc
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41		٠,	10	r (	-10-100-09B-6	ednen
4 C	9 0	₽.	455		-10-466-164-65	Sequence 65, Appl
		ላ ፡	289		-10-017-161	Sequence 2008, Ap
		4	289		8-10-292-798-165	Sequence 1654. An
44	35	84.2	344	6	US-09-898-570-18	guenc
45		4	344	10	US-09-839-446-18	, a
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RESULT 1						

US-09-761-636A-12

Sequence 12, Application US/09761636A

Sequence 12, Application US/09761636A

Sequence 12, Application US/09761636A

Sequence 12, Application US/09761636A

APPLICANT: STACKE, Steven

APPLICANT: CEDRROW, Angela

TITLE CENTROW, Angela

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48605 Achen et al.

CURRENT FILING DATE: 2000-01-018

PRIOR FILING DATE: 2000-01-018

PRIOR FILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-16

MUMBER OF SEQ ID NOS: 34

SEQ ID NO 12

LENGTH: 6

SEQ ID NO 12

LENGTH: 6

CORGANISM: Homo sapiens

US-09-761-636A-12

Query Match

Best Local Similarity 100.0%; Pred. No. 1.2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

ON 1 CVPLIC 6

DD 1 CVPLIC 6

ERSULT 2 US-10-424-599-164353 ; Sequence 164353, Application US/10424599 ; Publication No. US20040031072A1

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GRENEAL INFORMATION:
FILE REPERBENCE: 21402-218
FILE REPERBENCE: 21402-218
CURRENT APPLICATION UNDER: US/10/016,248
CURRENT FILING DATE: 2002-09-20
FRIOR PAPLICATION NUMBER: 60/291,037
FRIOR PAPLICATION NUMBER: 60/291,037
FRIOR APPLICATION NUMBER: 60/291,037
FRIOR APPLICATION NUMBER: 60/295,648
FRIOR APPLICATION NUMBER: 60/295,648
FRIOR APPLICATION NUMBER: 60/297,173
FRIOR APPLICATION NUMBER: 60/297,173
FRIOR PAPLICATION NUMBER: 60/309,258
FRIOR PAPLICATION NUMBER: 60/309,258
FRIOR PAPLICATION NUMBER: 60/309,268
FRIOR PAPLICATION NUMBER: 60/309,268
FRIOR APPLICATION NUMBER: 60/315,639
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-218
CURRENT APPLICATION NUMBER: US/10/016,248
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/254,329
                                                                                                                                                                                                                                                                                                              Score 36; DB 9; Length 613;
Pred. No. 3e+02;
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Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10016248
, Publication No. US20040033491A1
                                                                                                                                                                                                                                                                                                                      94.78;
83.38;
                                                                          1999-09-03
                           2000-08-29
                                                                                                                                  PatentIn Ver. 2.0
PRIOR APPLICATION NUMBER: E PRIOR FILING DATE: 2000-08-prior APPLICATION NUMBER: E PRIOR FILING DATE: 1999-09-NUMBER OF SEQ ID NOS: 19 SOFTWARE: Patentin Ver: 2.0
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Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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2486 CVPITC 2491
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                                                                                                                                                           SEQ ID NO 9
LENGTH: 613
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TITLE DE INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ar FILE REPERENCE: PT015P1
CURRENT APPLICATION NUMBER: US/09/799,514
CURRENT FILING DATE: 2001-03-07
                        APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-44-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 164353
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Sublication No. US20030017457A1

Sublication No. US20030017457A1

GENERAL INFORMATION:

APPLICANT: Fernandes, Elma R.

APPLICANT: Mishra, Vishnu S.

APPLICANT: Blinkets, Richard A.

APPLICANT: Schusen, Bryan D.

APPLICANT: Schusen, Bryan D.

APPLICANT: APPLICANT: Reduca, Ramesha

TILLE OF INVENTION: Novel Polynucleotides and Polypeptides Encoded Thereby

FILE REFERENCE: 15966-754

CURRENT PAPLICATION NUMBER: 2001-04-05

PRIOR PILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 60/195,576

WINDER: OF STATE 2000-04-06

WINDER: OF STATE 2000-04-06
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US-10-424-599-164353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 12;
Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 122
LENGTH: 175
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Sequence 9, Application US/09799514
Patent No. US20020065220A1
GENERAL INFORMATION:
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83.38;
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Matches 5; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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US-09-826-734-122
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US-09-826-734-122
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Score 36; DB 12; Length 3508;
Pred. No. 1.5e+03;
1; Mismatches 0; Indels (
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                                 PRIOR APPLICATION NUMBER: 60/254,329
PRIOR FILING DATE: 2006-12-08
PRIOR FILING DATE: 2001-12-08
PRIOR FILING DATE: 2001-05-15
PRIOR PAPLICATION NUMBER: 60/251,037
PRIOR FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: 60/255,648
PRIOR PILING DATE: 2000-06-08
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-0-01
PRIOR PILING DATE: 2001-0-01
PRIOR PILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PALENTIN VOWER: 2.1
SEQ ID NO 46
LENGTH: 3508
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Publication No. US20040033491A1
GENERAL INFORMATION:
                        2002-09-20
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Best Local Similarity 83.3
Matches 5; Conservative
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CRGANISM: Mus musculus
US-10-016-248-45
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                    CURRENT
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| Publication No. US20040101874A1
| GENERAL INFORMATION:
| APPLICANT: Ghosh, Edun D. |
| APPLICANT: Ghosh, Bing |
| APPLICANT: Glosh, Bradford W. |
| APPLICANT: Taylor, Steven W. |
| APPLICANT: Glosh, Bradford W. |
| APPLICANT: Glosh, Steven W. |
| APPLICANT: Glosh, Savy M. |
| APPLICANT: Marnock, Dale B. |
| TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION TITLE OF INVENTION INDERNEY. |
| TITLE OF INVENTION: G0088.465 |
| CURRENT APPLICANT: S003-04-04 |
| NUMBER OF SEQ ID NOS: 3077 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
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94.7%; Score 36; DB 12; Length 3389;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%; Score 36; DB 16; Length 3389; 83.3%; Pred. No. 1.5e+03; ive 1; Mismatches 0; Indels
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US-10-016-248-46
; Sequence 46, Application US/10016248
; Publication No. US20040033491A1
; Publication No. US20040033491A1
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/291,037
PRIOR FILING DATE: 2010-16-15
PRIOR FILING DATE: 2010-16-15
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-20-14
PRIOR FILING DATE: 2001-06-08
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-07-31
PRIOR PELICATION NUMBER: 60/326,393
PRIOR PILING DATE: 2001-10-01
PRIOR PILING DATE: 2001-10-01
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 167
SEQ ID NO 47
LENGTH: 3389
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Best Local Similarity 83.3
Matches 5; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 3389
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Sequence 663, Application US/10295027

Sequence 663, Application US/10295027

Sublication No. US20030232350A1

Sublication No. US20030232350A1

Sublication No. US20030232350A1

Sublication Aziz, Daniel

APPLICANT: Aziz, Natasha

APPLICANT: Ginsberg, Wendy M.

APPLICANT: Ginsberg, Wendy M.

APPLICANT: Ginsberg, Wendy M.

APPLICANT: Hevezi, Peter A.

APPLICANT: Marrian Richard

APPLICANT: Watson, Susan R.

APPLICANT: Watson, Susan R.

APPLICANT: Bos Biotechnology, Inc.

APPLICANT: Bos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, Chipspan Applicanton National Nations Nations Nations National Nations N
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US-09-983-025-25
; Sequence 25, Application US/09983025
; Publication No. US20030124529A1
; GENERAL INFORMATION:
; APPLICANT: OXVIG. Claus
; APPLICANT: OXVIG. Claus
; TITLE OF INVENTION: PREGNANCY-ASSOCIATED FLASMA PROTEIN-A2 (PAPP-A2)
; TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2 (PAPP-A2)
; TITLE OF INVENTION: DATE: 2001-10-22
; PRIOR PAPLICATION NUMBER: US 60/241,840
; PRIOR FILING DATE: 2000-10-20
; RIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 25
; NUMBER OF SEQ ID NOS: 25
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                                                          Score 35; DB 15; Length 31
Pred. No. 2.4e+02;
1; Mismatches 0; Indels
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Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0;
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PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PELING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1 SEQ ID NO 25
                                                                 Query Match 92.1
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapiens
US-09-983-025-25
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1410 CVPVTC 1415
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262 CLPLTC 267
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US-10-094-749-3057
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                                                       Sequence 198429, Application US/10424599
Sequence 198429, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: Are Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 198429
LENGTH: 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_21205C.1.pep
US-10-424-599-198429
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OTHER INFORMATION: unsure at all Xaa locations
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR PELING DATE: 2002-01-24
PRIOR PILING DATE: 2002-01-24
PRIOR PILING DATE: 2001-09-14
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Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAL, TAXAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUGIYAMA, TONOYASU
SUGIYAMA, TONOYASU
OTSUKI, TERSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
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OTSUKA, MOTOYUKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
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SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
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                                                       US-10-424-599-198429
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SOFTWARE: Patentin Ver. 2.1
                                           SEQ ID NO 3842
LENGTH: 570
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| Publication No. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Can Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Blants and Uses Thereof for Plant Improvement
| TITLE REPREBUCE: 38-21(53223)8 | CURRENT FILING DATE: 2003-04-28 |
| CURRENT FILING DATE: 2003-04-28 |
| NUMBER OF SEQ ID NOS: 285684 |
| SEQ ID NO 272858 |
| LENGTH: 80 |
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PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-012
PRIOR FILING DATE: 2002-01-10
PRIOR PLILOGATION NUMBER: US 60/347,349
PRIOR PLILOGATION NUMBER: US 60/355,250
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-03
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTHARE: PATENTIN VET: 2.1
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Pred. No. 1.1e+03;
1; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3842, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A010S
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE:
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_88413C.1.pep
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5, Conservative
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ORGANISM: Homo sapiens
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1410 CVPVTC 1415
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ORGANISM: Glycine max
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US-10-424-599-272858
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LENGTH: 162
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Patent No. 5208144
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Sequence 2, Appli
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Sequence 84,
Sequence 84,
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: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
: /cgn2_6/ptodata/2/iaa/pcTuS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-325-071-65

US-08-461-004A-65

US-08-325-071-59

US-08-325-071-67

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US-08-461-004A-59

US-08-461-004A-59

US-08-461-004A-63

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US-08-461-004A-63

US-08-461-004A-63

US-08-461-004A-63

US-08-461-004A-63

US-09-361-709B-3

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US-09-561-709B-1

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US-08-652-877-86
US-08-652-877-88
US-08-652-877-88
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                                                                                                     OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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38
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seq length: 200000000
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Match Length
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                                                                                                                                                               September
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Perfect score:
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4708
LENGTH: 159
Sequence 9, Appli
Sequence 5, Appli
Sequence 5, Appli
                                                   Sequence 5, Appli
Sequence 17751, A
Sequence 32545, A
Sequence 34, Appl
Sequence 24, Appl
Sequence 28, Appl
Sequence 28, Appl
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels
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Patent No. 5587311

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: CORON, Stewart Gary

APPLICANT: MOONE, Joanna Terry

APPLICANT: WILLADEN, Law Anthony York

APPLICANT: KEMP, David Harold

APPLICANT: RIBING, George Alfred

APPLICANT: RIBING, George Alfred

APPLICANT: RAND, Keith No. 558731man

TITLE OF INVENTION: DNA Encoding A Cell Membrane

TITLE OF INVENTION: Glycoprotein Of A Tick Gut

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:
                     US-08-033-873-5
US-08-033-873-5
US-08-356-822-5
US-09-252-991A-17751
US-09-252-991A-187751
US-09-252-991A-187751
US-09-252-991A-18777
US-09-252-991A-18777
US-09-252-991A-18777
US-09-265-59-34
US-09-565-534
US-09-661-468-34
US-09-561-468-34
US-09-540-824-28
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US-08-033-873-15
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Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Acinetobacter baumannii
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         RESULT 1
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SEE: Foley & Lardner: 3000 K Street, N.W. Washington, D.C.

ADDRESSEE:

STREET: CITY: Wa COUNTRY:

ZIP: 20007-5109 COMPUTER READABLE FORM:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.8%; Score 33; DB 3; Length 549
83.3%; Pred. No. 3.7e+02;
.ive 0; Mismatches 1; Indels
                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,004A
FILING DATE: 04-JUN-1995
PRIOR APPLICATION NUMBER: US 08/325,071
FILING DATE: 19-OCT-1994
PRIOR APPLICATION NUMBER: US 08/062,109
FRICATION NUMBER: US 07/926,368
FRICATION NUMBER: US 07/926,368
FRICATION NUMBER: US 07/926,368
PRIOR DATE: 07-JUL-1988
PRIOR DATE: 07-JUL-1988
FILING DATE: 07-JUL-1988
FILING DATE: 06-JUL-1988
FRICATION NUMBER: PCT/AUB7/00401
FRIUNG DATE: 27-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P12570
FILING DATE: 10-JUN-1987
FILING DATE: 27-NOV-1986
ATCORNEY/AGENT INFORMATION:
REFERENCE/ADENT INFORMATION:
NAME: REPERENCE/DOCKET NUMBER: 29,768
REFERENCE/OFCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 20,768
REFERENCE/OFCKET NUMBER: 20,768
REFERENCE/DOCKET NUMBER: 20,768
REFERENCE/OFCKET NUMBER: 20,768
REFERENCE/DOCKET NUMBER: 20,768
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APPLICANT: MOORE, Joanna Terry
APPLICANT: MOORE, Joanna Terry
APPLICANT: MILLADSEN, Law Anthony York
APPLICANT: KEMP, David Harold
APPLICANT: RISKAWTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RADIO, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
         ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: PER PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 65, Application US/08325071 Patent No. 5587311 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 549 amino acids
amino acid
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Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-461-004A-61
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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APPLICANT: COBON, Stewart Gary
APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: WILLADSEN, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: WILLADSEN, Peter
APPLICANT: RIBNG, George Alfred
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
                         COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
SOUTHARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-0-0-1993
PRIOR APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-MG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-MG-1992
PRIOR APPLICATION NUMBER: DCT/AUG1992
PRIOR APPLICATION NUMBER: PCT/AUG1992
PRIOR APPLICATION NUMBER: PCT/AUG1992
PRILING DATE: 16-0-MC-1987
FILING DATE: 15-0-MC-1987
FILING DATE: 15-0-MC-1987
PRILING DATE: 16-0-MC-1987
FILING DATE: 16-0-MC-1987
PRILING DATE: 16-0-MC-1987
PRILING DATE: 16-0-MC-1987
PRILING DATE: 16-0-MC-1987
PRILING DATE: 19-0-MC-1987
PRILING DATE: 19-0-MC-1987
PRILING DATE: 19-0-MC-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT: Stephen A: RESISTRATION NUMBER: 27-MOV-1987
PRICK PRILING DATE: RESISTRATION NUMBER: 27-MOV-1987
PRILING DATE: 17-MOV-1987
PRILING DATE: 17-MOV-1987
PRILING DATE: 19-0-MC-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT: Stephen A: RESISTRATION NUMBER: 27-MOV-1987
PRICK PRILING DATE: TOWNER: 27-MOV-1987
PRILING DATE: 27-MOV-1987
PRILING DATE: 19-0-MC-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT: Stephen A: RESISTRATION NUMBER: 27-MC-111 HIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPRAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: Foley & Lardner: 3000 K Street, N.W. Washington, D.C.
      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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         MEDIUM TYPE:
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Gaps

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86.8%; Score 33; DB 3; Length 620;
83.3%; Pred. No. 4.2e+02;
iive 0; Mismatches 1; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

APPLICATION
   APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60042/152
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
CMEDIUM TYPE: Floppy disk
CMEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFFLICHION NOMBEK: AN F12370
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AN PH9196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, SEEPHEN 29, 768
REFERENCE/DOCKET NUMBER: 60042/1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRENCE 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 56, Application US/08325071; Patent No. 5587311; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU PI2570
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-08-325-071-56
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                           CURENTIANG SYSTEM: WC-UCS/MS-DUS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: US/08/325,071
FILING DATE: US/08/325,071
FILING DATE: 1-A-OCT-1993
PRIOR APPLICATION NUMBER: US 08/062,109
FILING DATE: 1-A-MAY-1993
FILING DATE: 1-A-MAY-1993
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION NUMBER: PCT/AUB7/00401
FILING DATE: 10-AUC-1988
PRIOR APPLICATION NUMBER: AU P14912
FILING DATE: 12-AU0-1987
PRIOR APPLICATION NUMBER: AU P14912
FILING DATE: 15-AUN-1987
PRIOR APPLICATION NUMBER: AU P19196
FILING DATE: 19-AUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P19196
FILING DATE: 19-AUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P19196
FILING DATE: 19-AUN-1987
PRIOR APPLICATION NUMBER: AU P19196
FILING DATE: 19-AUN-1987
PRIOR APPLICATION NUMBER: AU PH9196
FILING DATE: 19-AUN-1987
PRIOR DATE: 19-AUN-1987
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 60042/111 BIAU TELECOMMUNICATION INFORMATION: TELEPHONE: 202 672 5300 TELEPHAK: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 65, Application US/08461004A
Patent No. 6235283
GENERAL INFORMATION:
APPLICANT: COGNON, Stewart Gary
APPLICANT: OGNISON, Law Anthony York
APPLICANT: JOHNSON, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                         E: Foley & Lardner 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3%,
Thes 5; Conservative
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                CITY: Washington, D.C.
                               NUMBER OF SEQUENCES: 7:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-325-071-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 CVPTTC 122
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US-08-461-004A-65
                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
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Gaps

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APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: WILLADSEN, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: WENP, David Harold
APPLICANT: RENP, David Harold
APPLICANT: RENP, George Alfred
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEV F. STREPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADJURES:
ADDRESSEE: FOOLY & Latcher
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 17-NAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-NAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU37/00401
FILING DATE: 10-CT-1997
PRIOR APPLICATION DATA: AD P14912
FILING DATE: 10-CT-1987
PRIOR APPLICATION DATA: AD P1916
FILING DATE: 10-CT-1987
PRIOR APPLICATION DATA: AN P1916
FILING DATE: 10-CT-1987
PRIOR APPLICATION DATA: AN P1916
FILING DATE: 10-CT-1987
PRIOR APPLICATION DATA: AN P1916
FILING DATE: 17-NOV-1986
ATTORNEY ADDITCATION DATA: AD P1916
FILING DATE: 27-NOV-1986
ATTORNEY ADDITCATION NUMBER: 29,768
ATTORNEY ADDITCATION NUMBER: 29,768
ATTORNEY ADDITCATION NUMBER: 29,768
ATTORNEY ADDIT NUMBER: 29,768
ATTORNEY ADDITCATION NUMBER: 29,768
ATTORNEY ADDIT NUMBER: 29,768
ATTORNEY ADDITCATION NUMBER: 20,768
ATTORNEY ADDITCATION NUMBER: 20,2672
ATTORNEY ADDITCATION NUMBER: 20,2672
ATTORNEY ADDITCATION NUMBER: 202672
ATTORNEY
                                                                         Sequence 59, Application US/08325071
Patent No. 5587311
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELBEAK: 204
TELER: 904136
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
"""R: amino acid
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-325-071-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 86.8%; Score 33; DB 1; Length 650; Best Local Similarity 83.3%; Pred. No. 4.4e+02; Matches 5; Conservative 0; Mismatches 1; Indels
APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: MILLADSEN, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: WILLADSEN, Peter
APPLICANT: REMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCES: 71
CORRESPONDENCES: Foley & Larcher
STREET: 3000 K Street, N.W.
CUTY: Washington, D.C.
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA

ZIP: 20007-5109

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AUB/100401
FILING DATE: 27-NOV-1987
PRIOR APPLICATION NUMBER: AU P14912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION NUMBER: AU P14912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION NUMBER: AU P14912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION NUMBER: AU P1997
FILING DATE: 19-UNN-1987
PRIOR APPLICATION NUMBER: AU P1996
FILING DATE: 27-NOV-1986
ATPCRNEY AGENT INFORMATION:
NUMBE: BENT STEPPEN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60042/111 BIAU
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29,768
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INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 650 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-325-071-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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ö Gaps 0 86.8%; Score 33; DB 1; Length 650; 83.3%; Pred. No. 4.4e+02; iive 0; Mismatches 1; Indels Query Match
Best Local Similarity 83.3
Matches 5; Conservative 147 CVPTTC 152 1 CVPLTC 6 qq à

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Gaps ; 0

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RESULT 7 US-08-325-071-59

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COMPUTER: USA

COMPUTER: CLAD

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC-DOS/MS-DOS

SOFTWARE: Batentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109

FILING DATE: 17-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/226,368

FILING DATE: 07-AUG-1992

PRIOR APPLICATION NUMBER: 07/242,196

FILING DATE: 07-AUG-1992

PRIOR APPLICATION NUMBER: O7/242,196

FILING DATE: 27-NOV-1987

PRIOR APPLICATION NUMBER: AU P14912

FILING DATE: 16-OCT-1987

PRIOR APPLICATION NUMBER: AU P14912

FILING DATE: 19-JUN-1986

PRIOR APPLICATION NUMBER: AU P12570

FILING DATE: 19-JUN-1987

PRIOR APPLICATION NUMBER: AU P1996

FILING DATE: 27-NOV-1986

APPLICATION NUMBER: AU P1997

PRIOR APPLICATION NUMBER: AU P18570

FILING DATE: 27-NOV-1986

ATPONEY/AGENT INFORMATION:
NAME: BENY, Stephen A.

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 20,768

REGISTRATION NUMBER: 60042/111 BIAU

TELEPHONE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA BROOding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
CORRESONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: JOHNSON, Law Anthony York
APPLICANT: WILLANSEN, Peter
APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
                                                                                                                                                          US-08-325-071-67
; Sequence 67, Application US/08325071
; Patent No. 5587311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 650 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3000 K Street, CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
147 CVPTTC 152
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                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington, D.C.
COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin NOWER: US/08/325,071
FILING DATE: 14-OCT-1993
RIOR APPLICATION NUMBER: US 08/062,109
FILING DATE: 07-AUG-1992
RIOR APPLICATION NUMBER: US 07/226,368
FILING DATE: 06-JUL-1988
FILING DATE: 27-NOV-1987
FILING DATE: 16-OCT-1987
RILING DATE: 16-OCT-1987
RILING DATE: 16-OCT-1987
RILING DATE: 16-OCT-1987
RILING DATE: 15-JUN 1987
RILING DATE: 15-JUN 1987
RILING DATE: 27-NOV-1986
FILING DATE: 27-NOV-1986
FILING DATE: 27-NOV-1986
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1987
ATTICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1987
ATTICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1987
AUGH19196
                                                                                                                                                                     APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: MOORE, Joanna Terry
APPLICANT: MILADSEN, Deter
APPLICANT: WILLADSEN, Deter
APPLICANT: KEMP, David Harold
APPLICANT: KEMP, David Harold
APPLICANT: RINKO, George Alfaed
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein of A Tick Gut
NUMBER OF SEQUENCES: J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60042/111 BIAU
          RESULT 8
US-08-325-071-63
Sequence 63, Application US/08325071
Patent No. 5587311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Foley & Lardner 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-325-071-63
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Gaps
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Pred. No. 4.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COWNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
CORPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,004A
FILING DATE: 04-04U1-1994
FILING DATE: 19-07-1994
FILING DATE: 19-07-1994
FILING DATE: 19-07-1994
FILING DATE: 10-07-1994
FILING DATE: 10-07-1994
FILING DATE: 10-07-109-1994
FILING DATE: 10-07-109-1995
FILING DATE: 10-07-109-1998
FILING DATE: 10-07-109-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MILLADSAN, FECEL
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrar
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60042/152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COBON, Stewart Gary
MOORE, Joanna Terry
JOHNSON, Law Anthony York
WILLADSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P12570
FILING DATE: 19-UW-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHON NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 59, Application US/08461004A
Patent No. 6235283
GENERAL INFORMATION:
APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: JOHNSON, Law Anthony YO
APPLICANT: WILLADSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
                                                                                                                              86.8%;
                                                                                                                                                            83.3%;
                                                                                               Query Match
Best Local Similarity 83.3°
"Thes 5; Conservative
                       MOLECULE TYPE: protein US-08-461-004A-56
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                         147 CVPTTC 152
                                                                                                                                                                                                                                                            1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-08-461-004A-59
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      Gaps
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      Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
COMPUTER: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: NG-104A
FILING DATE: US/08/461,004A
FILING DATE: US/08/461,004A
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/325,071
FILING DATE: 19-CCT-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: US-AVG-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/242,196
FILING DATE: 10-CVT-1987
PRICK APPLICATION DATA:
APPLICATION NUMBER: AU P14912
FILING DATE: 10-CVT-1987
PRICK APPLICATION DATA:
APPLICATION NUMBER: AU P14912
FILING DATE: 10-CVT-1987
PRICK APPLICATION DATA:
APPLICATION NUMBER: AU P12570
FILING DATE: 10-CVT-1987
PRICK APPLICATION NUMBER: AU P12570
FILING DATE: 10-CVT-1987
PRICK APPLICATION NUMBER: AU P12570
FILING DATE: 10-CVT-1987
PRICK APPLICATION NUMBER: AU P19196
FILING DATE: 11-CVT-1987
PRICK APPLICATION NUMBER: AU P19196
FILING DATE: 10-CVT-1987
PRICK APPLICATION NUMBER: AU P19196
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: COBON, Stewart Gary
APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: MILADSEN, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: WISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
          ä
          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60042/152
                                                                                                                                                                                                                                                                      US-08-461-004A-56;
; Sequence 56, Application US/08461004A.
Patent No. 6235283;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3000 K Street, N.W. Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
             5; Conservative
                                                                                                                                        147 CVPTTC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20007-5109
                                                                       1 CVPLTC 6
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             Matches
                                                                                                                                                                                                                                           RESULT 10
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,004A
FILING DATE: 104-01995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,071
FILING DATE: 19-04-1994
FILING DATE: 17-04-1993
RICH APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-04-1993
RICH APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-40G-1992
RICH APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-40G-1992
PRIOR APPLICATION NUMBER: US 07/926,368
FILING DATE: 06-40U-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU87/C
FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 CVPTTC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-08-461-004A-67
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0
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83.3%; Pred. No. 4.4e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUUNTY: WAS COUNTY: USA ZIP: 20007-5109 COUNTY: USA ZIP: 20007-5109 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE PERSONS PC-DOS/MS-DOS SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTING NUMBER: US/08/461,004A FLING DATE: 04-JUN-1995 APPLICATION DATA: APPLICATION NUMBER: AU PI1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: MOORE, Joanna Terry
APPLICANT: WILLADSEN, Law Anthony York
APPLICANT: WILLADSEN, Peter
APPLICANT: KEMP, David Harold
APPLICANT: RIDING, George Alfred
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 63, Application US/08461004A Patent No. 6235283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P12570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: AU PI4912
16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
                                                                                                        : 650 amino acids
amino acid
                     TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3
Matches 5; Conservative
  202 672 5399
                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-461-004A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                          147 CVPTTC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: COBON,
                                                                                                                                                                                                                                                                                                                                                                         1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-461-004A-63
TELEFAX:
                                                                                                  LENGTH:
                                                                                                                                   TYPE:
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NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 60042/152
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5399
TELEFAX: 202 672 5399
                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
                                                                                                                                                                                                                             ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-004A-63
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. 0

Gaps

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Score 33; DB 3; Length 650; Pred. No. 4.4e+02; 0; Mismatches 1; Indels

Sequence 67, Application US/08461004A Patent No. 6235283

GENERAL INFORMATION:
APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE, Joanna Terry
APPLICANT: MOORE, Joanna Terry
APPLICANT: WILLADSEN, Peter
APPLICANT: WILLADSEN, Peter
APPLICANT: KEMP, David Harold
APPLICANT: RIPRO, George Alfred
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: SIYCOPTOCION OF A TICK GUT
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS: STREET: 3000 K Street, N.W. CITY: Washington, D.C. COUNTRY: USA Foley & Lardner

PCT/AU87/00401

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Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: COBON, Stewart Gary
APPLICANT: COBON, Stewart Gary
APPLICANT: MOORE Joanna Terry
APPLICANT: MILLADSEN, Peter
APPLICANT: RIBLADSEN, Peter
APPLICANT: REBY, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,004A
FILING DATE: 04-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,071
FILING DATE: 19-OCT-1994
PRIOR APPLICATION PARE:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
                                        FILING DATE: 16-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 40 P12570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU F19196
FILING DATE: 27-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 20,768
TELECHOMINICATION INFORMATION:
TELEPHONE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/926,368 FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-461-004A-57; Sequence 57, Application US/08461004A; Patent No. 6235283
                     APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO: 57
SEQUENCE CHARACTERISTICS:
LNGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 CVPTŤC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CVPLTC 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 57, Application US/08325071
; Sequence 57, Application US/08325071
; Patent No. 5587311
; GENERAL INFORMATION:
APPLICANT: MCORE, Joanna Terry
APPLICANT: WCORE, Joanna Terry
APPLICANT: WILLADSEN, Peter
APPLICANT: KILLADSEN, Peter
APPLICANT: KILLADSEN, Peter
APPLICANT: KILLADSEN, Peter
APPLICANT: RAND, George Alfred
APPLICANT: RAND, Keith No. 5587311man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURREALING SISIENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-0CT-1993
PRICH APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRICH APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-MG-1992
PRICH APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-MG-1992
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/242,196
FILING DATE: 06-UUL-1988
PRICH APPLICATION DATA:
APPLICATION DATA: 27-NOV-1997
FILING DATE: 27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 3; I
Pred. No. 4.4e+02;
0; Mismatches 1;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI2570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA: 40-1986
APPLICATION NUMBER: AU PH9196
FILING DATE: 27-NOV-1986
ATTORNEY, AGENT INFORMATION:
NAME: BENY, SLEEDER A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/152
TELECOMMUNICATION:
TELECHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington, D.C.
CCUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: Foley & Lardner: 3000 K Street, N.W. Washington, D.C.
                                                                                                                                                                                                                                                                                                         TELEX: 904136
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-461-004A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 CVPTTC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CVPLTC 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-325-071-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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86.8%; Score 33; DB 3; Length 688;
83.3%; Pred. No. 4.6e+02;
tive 0; Mismatches 1; Indels
APPLICATION NUMBER: 07/242,196
FILING DATE: 06-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AUB7/00401
FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: W P14912
FILING DATE: 16-OCT-1987
PRIOR APPLICATION NUMBER: AU P12570
FILING DATE: 19-JUN-1987
PRIOR APPLICATION NUMBER: AU P9196
FILING DATE: 27-NOV-1986
F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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Gaps 0;

Search completed: September 5, 2004, 10:22:00 Job time : 6.33333 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

September 5, 2004, 09:47:29; Search time 7.67677 Seconds (without alignments) 125.302 Million cell updates/sec Run on:

US-09-761-636A-13 56 1 CISVPLSVPC 10 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

283366

seq length: 0 seq length: 200000000 Minimum DB & Maximum DB &

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	al procession of the processio	hypothetical prote hypothetical prote
SUMMARIES		
SUMM	144555 G82599 G82599 JC46999 JC49999 D71864 A33621 A33621 B96731 G83136 G83136 G83136 H96745 F72751 T15039 T15039 T15039 T15039 T15039 A70817 A70817 A70817	7211
DB	000000000000000000000000000000000000000	1 73
Length	$\omega_{4,0}$ 0488800004880004758000775807	759
% Query Match	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	
Score	<b>ﺳ ﮐﯿ </b>	35
sult No.	0 4 6 7 8 8 9 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	29

hypothetical prote	agitoxin 3 - scorp	hypothetical profe	probable PTS syste	requiatory protein	regulatory protein	hypothetical prote	probable secreted	hypotherical prote	dene Brn-3b profei	transcription fact	Drotpin C (activat	hymothetical prote	hypothetical prote	propanediol dehydr
B97852	C54471	H71023	AD0966	S06314	B33538	F89914	T44873	AD2559	138502	I48291	KXHU	C95349	H85135	JE0303
01	7 (	7	8	N	~	~	~	~	7	7	М	N	7	7
1162	38	156	249	250	252	328	387	399	410	440	461	502	527	554
62.5	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7
35	2, C.	34	34	34	34	34	34	34	34	34	34	34	34	34
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Н	
SULT	

hypothetical protein PA0631 [imported] - Pseudomonas aeruginosa (strain PAO1)

Cispecies: Pseudomonas aeruginosa Cipate: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 06-Oct-2000 Cipate: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 06-Oct-2000 Cipatession: T44555; B8358 Rivakayama, K.; Takashima, K.; Ishihara, H.; Shinomiya, T.; Kageyama, M.; Kanaya, S.; Ob Submitted to the EMBL Data Library, August 1999 A;Description: Genetic relationship between bacteriocins and bacteriophages. A;Reference number: Z22790

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rosidues: 1-85 cANA.
A;Cross-references: EMBL:AB030825; PIDN:BAR83170.1
A;Experimental source: strain PAO!
B;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
A;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
Adman, S.; Yuan, Y.; Brody, L.D.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
A;Stelence number: A82950; MUID:20437337; PMID:10984043
A;Atelence number: BB3568
A;Atelence number: BB358
A;Status: preliminary
A;Molecule type: DNA
A;Reidues: 1-65 cSTO>
A;Reperimental source: strain PAO!
A;Experimental source: strain PAO!

A; Gene: PA0631 Genetics

DB 2; Length 85; 1; Indels Score 39; DB 2 Pred. No. 6; 2; Mismatches h 69.6%; Similarity 66.7%; 6; Conservative 2 Query Match Best Local Similarity Matches 6; Conserv

0;

Gaps

; 0

: |||:||| 27 VEVPLAVPC 35 2 ISVPLSVPC 10 ò g

## RESULT 2 G82599

hypothetical protein XF2118 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000
C;Accession: G82599
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below

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Appeaription: provides precursors for DNA and RNA biosynthesis; it catalyzes the convex c'superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog c'steywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis pronses amino-terminal homology ciphomain: IMP dehydrogenase amino-terminal homology cIDHN>
F:172-220/Domain: CBS homology cBS2-8F:221-465/Domain: IMP dehydrogenase catalytic homology cIMP>
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hypothetical protein jhp0985 - Helicobacter pylori (strain J99)
hypothetical protein jhp0985 - Helicobacter pylori (strain J99)
kjpecies train J99
cjpecies train J99
cjpecies train J99
cjpate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
cjpate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
cjpate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
cjpate: 12-Feb-1999
cjpates C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Alterious caquence comparison of two unrelated isolates of the human gastric pat A;Accession: D71864
A;Accession
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A;Experimental source: strain J99
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C,Species: Xylella fastidiosa
C,Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: F82521
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
Osipiuk, J.; Trent, J.; Olsen, G.J.; Huberman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.9%; Score 38; DB 1; Length 503; 85.7%; Pred. No. 51; ive 1; Mismatches 0; Indels
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Pred. No. 6.
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C;Complex: homotetramer
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77.8%;
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Matches 6; Conservative
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A;Status: preliminary
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A;Gene: jhp0985
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Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arac-2001
Cispecies: Resolution (Cispecies)
Cispecies: Rar-2001
Cispecies: Rar-2001
Cispecies: Arac-2001
Cispecies: Arac-2002
Cispecies: Arac-2003
Cispeci
                                                                                                                                                                                     A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
B;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A B;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A siones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.; Franca, S.C.; Franco, M.C.; Frohm S.; Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, J.S.; Franca, S.C.; Franco, M.C.; Frohm Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, E.G.; Munes, L.R.; C.; Nurse, M.C.; Frohm Rodrigues, W.; Rosa, A.J. de M.Y.; Macoca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.; Rodrigues, W.; Rosa, A.J. de M.; de Rosa U.Y.; W.B.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaira A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaira A.C.R.; da Silvaira, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A.; Contents: annotation
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C;Keywords: GMP biosynthesis; NAD; oxidoreductase
                                                                                                                                                          A; Cross-references: GB: AE004026; GB: AE003849; NID: 99107228; PIDN: AAF84917.1; GSPDB: GN001
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JC4999
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Pred. No. 51;
1; Mismatches
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Pred. No. 10;
3; Mismatches
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50.0%;
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Best Local Similarity 50...
S; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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8 CCAVPMNAPC 17
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                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <SIM>
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A.Cross-references: GB M30691, NID:g205251; PIDN:AAA41548.1; PID:g205252
A; Experimental source: clone RK11
C; Superfamily: Ly-6 antigen; Ly-6 homology
C; Superfamily: Ly-6 antigen; Ly-6 homology
C; Superfamily: Ly-6 antigen; Ly-6 homology
F; 1-26/Domain: signal sequence #status predicted <SIG>
F; 1-26/Domain: signal sequence #status predicted <AMT>
F; 105/Product: Ly6 homolog RK3 #status predicted <AMT>
F; 106-134/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F; 105/Wodified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
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T.; Zalewski, C.; Ma
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A;Experimental source: strain R1
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C.Species: Deinococcus radiodurans
C.Species: 03-Dec. 1999 #sequence_revision 03-Dec. 1999 #text_change 17-Mar-2000
C.Accession: G75515
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A.;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans PA; Reference number: A75250; MUID:20036896; PMID:10567266
A.Stetus: preliminary
A.Molecule type: DNA
A.Residues: 1-256 <WHIS
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A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C'Species: Lactococcus lactis subsp. lactis
C'Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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Pred. No. 48;
3; Mismatches
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60.0%;
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55.6%;
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128 CINLPLQIP 136
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Matches 6; Conserv
A; Residues: 2-134 <FR2>
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Best Local Similarity
Matches 5; Conserv
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Cipecies: Volvox carteri
Cipate: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jul-2000
Cipate: 11-Apr-1990 #sequence_revision 11-Apr-1990
Cipate: 11-Apr-1990
Cipate: No. 1990
Cipate: No. 19
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Ly6 homolog RK3 precursor - rat

Ly6 homolog RK3 precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Species: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 31-Jan-2000

C;Accession: D45835; C45835

R;Rriedman, S.; Palfree, R.G.E.; Sirlin, S.; Haemmerling, U.

A;Title: Analysis of three distinct Ly6-A-related cDNA sequences isolated from rat kidne

A;Reference number: A45835; MUID:90152758; PMID:2154400

A;Residues: 1-134 cFRI>
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A;Residues: 1-485 <ERT>
A;Cross-references: GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C;Keywords: glycoprotein
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66.1%; Score 37; DB 60.0%; Pred. No. 73;

2; Mismatches

6; Conservative 1 CISVPLSVPC 10 | :|||: || CQTVPLTEPC 92

Best Local Similarity Matches 6; Conserv

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Query Match

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A; Molecule type: DNA
A; Residues: 1-89 <SIM>
A; Tooss-references GB.AED04080; GB.AED03849; NID:g9107971; PIDN:AAF85521.1; GSPDB:GN001
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Asrinese, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.S.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A; Authors: Ferreira, W.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Largrado, M.A.; Madeira, A.M.B.N.; Madeira, H.W.; Martino, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.E.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawasak A, Authors: ad Silva, A.C.R.; da Silva, M.C.; da Silva, M.S.; Silva Jr., W.A.; da Silvain, M.D. Franco, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
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Mismatches

Conservative

Query Match Best Local Similarity 6, Conserve

A; Gene: XF2736

C, Genetics

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2 ISVPLSVPC

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VSAPLRVPC 27

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A;Molecule type: DNA
A;Residues: 1-581 <DU2.
A;Cross-references: EMBL:U00062; NID:g488162; FIDN:AAB68911.1; PID:g488176; MIPS:YHR032v
C;Genetics:
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A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop)
A; Reference number: A72450; MUID: 99310339; PMID: 10382966
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A,Map position: 1
A;Introns: 75/3; 94/3; 131/3; 171/3; 207/3; 266/2; 299/3; 323/1; 505/1; 528/1; 612/3
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F72751
                    hypothetical protein YHR032w - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein H8179.15
C,Species: Saccharomyces cerevisiae
C,Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 19-Apr-2002
C,Accession: S46742
S;Du, Z.
Submitted to the RMBL Data Library, May 1994
A,Description: The sequence of S. cerevisiae cosmid 8179.
A,Reference number: S46732
A,Accession: S46742
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A,Map position: 8R
C,Keywords: transmembrane protein
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Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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564 CVSIPVSSGC 573
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-100 < KAW>
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                                                                                                                                                                                                                                        probable amino acid permease PA4072 [imported] - Pseudomonas aeruginosa (strain PA01) probable sumino acid permease PA4072 [imported] - Pseudomonas aeruginosa (strain PA01) C.Species: Pseudomonas aeruginosa (c.Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C.Accession: G83136 C.Accession: G83136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Circlesion: H96792
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 406, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Winn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: Assistance of chromosome 1 of the plant Arabidopsis.
A;Reference number: Assistance of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable steroid 22-alpha-hydroxylase T9L24.44 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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C,Superfanily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C,Keywords: heme; iron; metalloprotein
F;455/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Realdudes: 1-512 <STO>
A;Cross-references: GB:AE005173; NID:g11120803; PIDN:AAG30983.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 496;
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Pred. No. 1.1e+02;
3; Mismatches 2; Indels
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illarity 50.0%;
Conservative 3
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345 CIAVAAAIPC 354
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244 CLSVPIDLP 252
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CISVPLSVPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA78912.1; PID:g5103391
A;Experimental source: strain Kl
C;Genetics:
A;Gene: APE0003
C;Superfamily: Aeropyrum pernix hypothetical protein APE0003
```

Query Match 62.5%; Score 35; DB 2; Length 100; Best Local Similarity 71.4%; Pred. No. 35; Matches 5; Conservative 2; Mismatches 0; Indels

0; Gaps

0;

4 VPLSVPC 10 :||:||| 57 IPLTVPC 63

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Search completed: September 5, 2004, 10:01:24 Job time : 9.67677 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 5, 2004, 09:38:39 ; Search time 4.54545 Seconds (without alignments)
114.554 Million cell updates/sec Run on:

US-09-761-636A-13 56 1 CISVPLSVPC 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		piromyces	Oggaza arabidonoio	arabidon		P51986 chlorohydra		sacchai	_									homo		vibrio f			dictv					pan t	pirc		homod	pan t	013092 saimiri bol
SUMMARIES	ID	MANC DIRED		1		Y396 HELPJ	CG2A_CHLVR	SGP_VOLCA	YHJ2_YEAST	COTE_HUMAN	MA2_MYCBO	MAFB_HUMAN	MAFB_MOUSE	MAFB_RAT	181_FOWPV	FD21_MYCTU	D21 MYCLE	CH2_CANFA	SY23_HUMAN	SCA3_LEIQH	JXR_VIBFI	V027 FOWPV	PO42_HUMAN	rc1_bicbi	RIC HUMAN	DHAB_SALTY	MP44_SFVKA	ILL HUMAN	ILL PANTR	ANA PIRSP	CADG HUMAN	OPSB_HUMAN	OPSB PANTR	OPSB_SAIBB
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P54844 rattus norv P23091 avian muscu P54843 mus musculu 075444 homo sapien Q14153 homo sapien P53101 saccharomyc Q91vu6 mus musculu P19467 mus musculu Q50586 mycobacteri P58021 mus musculu Q58021 mus musculu Q58051 homo sapien P16044 tachypleus
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4 2 1 NFEEDENR
RAT MOUSE HUMAN TEAST MOUSE MO
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369 369 370 465 465 573 663 663 663
<u> </u>
588 588 599 599 598 598 598 598 597 11.
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## ALIGNMENTS

DB 1; Length 569;

75.0%; Score 42;

Query Match

502 AA.

PRT;

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Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                    16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable inosine-5'-monophosphate dehydrogenase (BC 1.1.1.205) (IMP
dehydrogenase) (IMPDH) (IMPD).
                                  40, Created)
            STANDARD;
                                                                                dehydrogenase) (IMPDH
ATIG16350 OR F309.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 3
502 AA;
                                16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
                                                                                                                                                 NCBI TaxID=3702;
IMH2_ARATH
ID _IMH2_ARATH
AC _Q9SA34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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              ö
                                                                                                                                                                                                                                                                                                                  "Evidence that the Piromyces gene family encoding endo-1,4-mannanases arose through gene duplication.";
FEMS Microbiol. Lett. 141:183-1865.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic linkages in mannans, galactomannans, glucomannans, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                             galactoglucomannans.
--- SIMILARITY: THE 39 AA REPEATS ARE SIMILAR TO THOSE IN MANA, MANC AND XYNA, AND TO THOSE OF N.PATRICIARUM XYNA.
--- SIMILARITY: Belongs to family 26 of glycosyl hydrolases.
               Gaps
                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
15-UTL-1998 (Rel. 36, Last annotation update)
Mannan endo-1,4-beta-mannosidase B precursor (EC 3.2.1.78) (Beta-mannanase B) (1,4-beta-D-mannan mannanohydrolase B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MANNAN ENDO-1,4-BETA-MANNOSIDASE B. 2 X 39 AA APPROXIMATE REPEATS.
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Pred. No. 4.4;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=96313314; PubMed=8768520;
Millward-Sadler S.J., Hall J., Black G.W., Hazlewood G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Glycosidase; Signal; Multigene family; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                 Indels
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                                                                                                                                                                                                                        Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
Neocallimasticaceae; Piromyces.
NCBL_TaxID=45796;
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    Pred. No. 4.3;
                  Mismatches
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InterPro; IPR009034; Dockering CDD.
InterPro; IPR008979; Gal bind like.
InterPro; IPR008095; Glyco hydro_26.
Ffam; PF02013; CBM_10; 2.
Ffam; PF02156; Glyco hydro_26; 1.
PRINTS; PR00739; GLHYDRIASE26.
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      60.08;
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                  Conservative
                                                                                                                        STANDARD;
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                                                               490 ČFŠIPĽGYPČ 499
                                         10
                                         1 CISVPLSVPC
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    Best Local Similarity
Matches 6, Conserv
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                                                                                                                     MANB PIRSP
P55297;
                                                                                                                                               01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                              MANB PIRSP
                                                                                                  RESULT 2
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                                                                                                                                                                                                 use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC006341; AAD34687.1; -.

PIR; P86298; R86298.

HSSP; P12268; 1B30.

InterPro; IPR001099; FMN_enzyme.

InterPro; IPR001093; IMPDh/GMPRtase.

Pfam; PP00478; IMPDH; 1.

TIGREAMS; TIGR01302; IMP dehydrog; 1.

PROSITE; PS00487; IMP GMP RED; 1.

Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
"ALTE 408:816-820(2000).

"ALTE 408:816-820(2000).

-!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O = xanthosine 5'-phosphate + NADH.

-!- PATHWAY: First reaction unique to GMP biosynthesis.
-!- SIMILARITY: Belongs to the IMPDH/GMPR family.
-!- SIMILARITY: Contains 1 CBS domain.
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1; Mismatches
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Best Local Similarity
Matches 6; Conserv
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49 VPLSIPC
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RESULT 3

us-09-761-636a-13.open.rsp

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CBS domain.
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SEQUENCE
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SC STRAIN=cv. Columbia,

RA MEDINE=21016719; PubMed=11130712;

RA Mologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Mite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyuw T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkrins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Lee A., Lee J.M., Neuran W.C., Osborne B.I.,

RA Langin-Hooper S., Low A., Lurso J.S., Maiti R., Marziali A.,

RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Utterback T., Van Aken S., Vasberg M., Wysotskaia V.S., Walker M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.

NCBI_TaxID=3702,
                                                                                                                                                                                                                                                                                                                                       Collart F.R., Osipiuk J., Trent J., Olsen G.J., Huberman E.; "Cloning and characterization of the gene encoding IMP dehydrogenase from Arabidopsis thaliana."; Gene 174:217-220(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 408:816-820(2000).
-!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O xanthosine 5'-phosphate + NADH.
-!- PATHWAY: First reaction unique to GMP biosynthesis.
-!- SIMILARITY: Belongs to the IMPDH/GMPR family.
-!- SIMILARITY: Contains 2 CBS domains.
                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
Inosine-5-monophosphate dehydrogenase (EC 1.1.1.205) (IMPDH OR ATIG79470 OR T8K14.11.
                                                          503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR003009; FMN enzyme.
InterPro, IPR005990; IMP dehyd.
InterPro, IPR001093; IMPDh/GMPRtase.
Pfam, PF00478; IMDDH, I TIGRFAMS, TIGR01302; IMP dehydrog; I
PROSITE; PS00487; IMP DH_GMP_RED; I.
                                                          PRT;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE=97045815; PubMed=8890737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC007202; AAD30229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L34684; AAB41940.1;
                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; JC4999; JC4999.
HSSP; P12268; 1B30.
                                                       IMH1_ARATH
P47996;
                      RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99120557; PubMed=9923682; Alm R.A. Ling L.S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., dedonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-!- SIMILARITY: Belongs to the ubiD family.
                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                   Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 1; Length 616;
Pred. No. 24;
                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                   503 AA; 54194 MW; ADDDAF9C3A697A9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 616 AA; 70989 MW; C219BIDCE4C8BDD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                 DB 1;
20;
                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein JHP0985.
IMP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CALOrohydra viridissima (Hydra).
                                                                                                                                                                                                                                                                                                                            616 AA.
                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                              67.9%; Score 38; 85.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; D71864; D71864.
InterPro; IPR002830; carboxylyase.
Pfam; PP01977; UbiD; 1
TIGRFAMS; TIGR00148; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE001527; AAD06568.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.9%;
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 77.8
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 CLŚNPLSVP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                        4 VPLSVPC 10
                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVPLSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=85963;
                                                                                                                                                                                       |||||||
49 VPLSIPC
                                                                                                                                                                                                                                                                                                                  Y396 HELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG2A CHLVR
P51986;
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
STRAIN=S288C / AB972;
STRAIN=S288C / AB972;
MEDLINE=943708003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston M., Andrews S., Brinkman S., Geisel C., Kirsten J.,
Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 265:2077-2082(1994).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the multi antimicrobial extrusion (MATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accharomyces cerevisiae (Baker's yeast).
Saccharopta, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
PTM: Hydroylated on proline residues in the Pro-rich central
                                                                                                                                                                                                                                                                                                                                                                                 POLY-PRO. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                   POTENTIAL.
SULPATED SURPACE GLYCOPROTEIN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FBB-1995 (Rel. 31, Created)
01-FBB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical 64.2 kDa protein in SLT2-PUT2 intergenic region.
                                       contains sulfate-substituted glycans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            A52216400A031421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           581 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                               PRO-RICH.
                                                                                                                                                                                                                                                                                                  Signal; Glycoprotein; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   50436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U00062; AAB68911.1; -.
PIR; S46742; S46742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.1%;
60.0%;
                                                                                                                                                                                                                                                          EMBL; X51616; CAA35953.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                            485
340
295
193
347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|||: ||
83 CQTVPLTEPC 92
                                                -!- PTM: Glycosylated;
                                                                                                                                                                                                                                                                                                                                            21
228
360
193
347
485 AA;
                                                                                                                                                                                                                                                                                  PIR; A33647; A33647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHJ2 YEAST
P38767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family
                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YHJ2_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
      à
                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Polymer.
PTM: Intersubunit cross-links are formed between saccharide chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the cellular compartment.";
J. Cell Biol. 109:3493-3501(1989).

-i. FUNCTION: The extracellular matrix (ECM) of volvox contains insoluble fibrous layers that surround individual cells at a distance to form contiguous cellular compartments. SSG 185 is the monomeric precursor of this substructure (C3Z structure).
                                                                                                                                                                                                        J. Cell Sci. 109:1063-1069(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οŧ
                                                                                                                                                                                                                                           (mitosis) translition. Interacts with the CDC2 and CDK2 protein kinases to form MPF. G2/M cyclins accumulate steadily during G2 and are abruptly destroyed at mitosis (By similarity).
                                                                                                                                                                               "Presence and expression of G2 cyclins in the coelenterate hydra.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=f. Nagariensis / HK10;
STRAIN=f. Nagariensis / HK10;
Brill H., Mengele R., Wenzl S., Engel J., Sumper M.;
The extracellular matrix of Volvox carteri: molecular structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
             Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                                                                                                                        MEDLINE=96338615; PubMed=8743953;
Scheurlen-Blchle I., Hoffmeister S., Herrmans-Borgmeyer I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulfated surface glycoprotein 185 precursor (SSG 185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 AA; 47989 MW; 79225BF8D1B44788 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 1;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 19, Created)
(Rel. 19, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMRT; SW0385; CYCLIN; 2.
PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rather than between polypeptide chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006670; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
InterPro; IPR006671; Cyclin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.1%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00134; cyclin; 1. Pfam; PF02984; cyclin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X90983; CAA62470.1; -. HSSP; P30274; IVIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408 CVSSLVPLEMPC 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CIS--VPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                         Hydridae; Chlorohydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Volvocaceae; Volvox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3067;
                                                           NCBI_TaxID=6082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Volvox carteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991
01-AUG-1991
15-MAR-2004
                                                                                                                                                                       Schaller H.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VOLCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Hippocampus;
MEDLINE=97474796; PubMed=9331372;
Winfield S.L., Tayebi N., Martin B.M., Ginns E.I., Sidransky E.;
"Identification of three additional genes contiguous to the
glucocerebrosidase locus on chromosome 1q21: implications for Gaucher
disease.";
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- TISSUE SPECIFICITY: Widely expressed.
-!- SIMILARITY: TO HUMAN KIAA0574.
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                                                                                                                                                                                                                                                                                                                              Score 36; DB 1; Length 581;
Pred. No. 53;
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Pred. No. 61;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                          B0592C480589319B CRC64;
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                                                                                                                            Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      669 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; T08827; T08827.
Genew; HGNC:1233; Clorf2.
GO; GO:0016021; C:integral to membrane; NAS.
                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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POLY-SER.
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                                                                                                                                                                                                                                                                          64209 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF023268; AAC51822.1; -.
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                                                                                               TIGRFAMS; TIGR00797; matE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 7:1020-1026(1997)
                                                                                                                                                                                                                                                                                                                              64.38;
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70.0%;
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GermOnline; 139349; -.
SGD; S0001074; YHR032W.
InterPro; IPR002528; MatE.
Pfam; PF01554; MatE; 2.
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50 (
Matches 5, Conservative
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564 CVSIPVSSGC 573
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87
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194
250
639
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                                                                                                                       Hypothetical protein;
TRANSMEM 173 193
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                                                                                                                                                                                                                                                                             581 AA;
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635
669 AA;
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282
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COTE_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Le Beau M.M.;
"Human KRWL (WAFB): cDNA cloning, genomic structure, and evaluation as
a candidate tumor suppressor gene in myeloid leukemias.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                 from
                                                                                                                                                                                                                                                                                                                      Mathur M., Kolattukudy P.E.;
"Molecular cloning and sequencing of the gene for mycocerosic acid
"Molecular cloning and sequencing of the gene for mycocerosic acid
"Mycobacterium tuberculosis var. bovis Bacillus Calmette-Guerin.";
J. Biol. Chem. 267:19388-193395(1992).
-!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV1521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Y5G3; Q9HIPI;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Transcription factor MafB (V-maf musculoaponeurotic fibrosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang P.W., Eisenbart J.D., Cordes S.P., Barsh G.S., Stoffel M.,
                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 1.
Hypothetical protein; Transmembrane.
SEQUENCE 298 AA; 32286 MW; 22232DD5DBC6F371 CRC64;
                                                                                                                                                                                                                         Corynebacterineae; Mycobacteriaceae; Mycobacterium
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                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 32.3 kDa protein in mas 5'region.
                                                                                           298 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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Pred. No.
                                                                                           PRT;
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                                                                                                                                                                                                                                                                                        STRAIN=BCG;
MEDLINE=92406887; PubMed=1527058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Bone marrow;
MEDLINE=99375320; PubMed=10444328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 62.5%;
Local Similarity 87.5%;
Les 7; Conservative
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                                                                                         STANDARD;
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      139 CPSVPLLRPC 148
                                                                                                                                                                                          Mycobacterium bovis.
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                                                                                                                                                                                                                                          NCBI_TaxID=1765;
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                                                        RESULT 10
YMA2_MYCBO
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Matches
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Best Local Similarity 70.0 Matches 7; Conservative

Genew; HGNC:6408; MAFB.

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                                         REP RECURS FROM N.A.

REP MEDLINE=21638749; PubMed=11780052;

RED MEDLINE=21638749; PubMed=11780052;

RED Deloutkas D., Matchews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Basley O.P., Bird C.P., Balakey S.E., Bridgeman A.M., Brown A.J.,
RA Basley O.P., Bird C.B., Butler A.P., Carder C., Carter N.P.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Grafham D.V., Griffiths C.D., Garlifths M.N.D., Gwilliam R.,
RA Hammond S., Harley J.L., Heath P.D., Hoo S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Hoo S., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Johnson D.,
RA Milne S.A., Mistry A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Milne S.A., Mistry D., Mocre M.J.F., Millikin J.C., Nickerson T.,
RA Rice C.M., Ross M.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Soderlund C., Steward C.A., Sulston J.E.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wall B. J., Williams S.A.,
Whitning L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Berk S.,
RA Rogers J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
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Genomics 59:275-281(1999).
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ACAINTENTRY IN INCOME LAND TO THE ACAINT OF 
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01-0CT-1996 (Rel. 34, Last sequence update)
15-MRA-2004 (Rel. 43, Last annotation update)
Transcription factor MafB (V-maf musculoaponeurotic fibrosarcoma oncogene homolog B) (Transcription factor MAFI) (Segmentation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The mouse segmentation gene kr encodes a novel basic domain-leucine zipper transcription factor."; cell 79:1025-1034(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                 GO: GO: 0005634; C:nucleus; TAS.
GO: GO: 0007423; P:sensory organ development; TAS.
InterPro: IPR004821; FE bill.
InterPro: IPR004826; TF Maf.
InterPro: IPR004826; TF Maf.
Pfam; PF03131; bill Maf. 1.
PROSITE; PS50217; BILI. 1.
PROSITE; PS50217; BILI. 1.
PROSITE; PS50036; BILI. 1.
PROSITE; PS00036; BILI. 1.
PROSITE; P
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 43;
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Q -> H (IN REF. 1).
AOF3C09F8936CB16 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                  LEUCINE-ZIPPER.
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0; Mismatches
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MEDLINE=95094266; PubMed=8001130;
                                                                                                                                                                                                                                                                                                                                                                                                                                 131 143 POI
158 167 POI
52 52 A -
241 241 Q -
323 AA; 35792 MW; A
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STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.v.
6; Conservative
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MAFB OR MAF1 OR KRML.
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MAFB MOUSE
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maf related genes: specific expression in chondrocytes, lens and
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131 1
158 1
194 2
323 AA;
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1D V181 FOWPV

AC Q9J552;
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                                          RAH TARAH TA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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PIR; 149529; 149529.
TRANSFAC; 701439; -.
MGD; MGI:104555; Matb.
GO; GO:0003677; F:DNA binding; IDA.
GO; GO:0003779; P:segmant specification; IMP.
InterPro; IPR004927; TF_DIP.
InterPro; IPR004927; TF_DIP.
FEGIP.
FEGI
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Plays a pivotal role in regulating lineage-specific hematopolesis by repressing ETG1-mediated transcription of erythroid-specific genes in myeloid cells.

-!- SUBCELLULAR LOCATION: Nuclear.

-!- TISSUE SPECIFICITY: MOST ABUNDANT IN KIDNEY, GUT, LUNG, AND BRAIN.

-!- DEVELOPMENTAL STAGE: DETECTABLE AT 8.0 DPC (ONE SOMITES) A BAND IN THE CAUDAL HINDBRAIN, AND BY 8.5 DPC (SIT OF SIGHT SOMITES), THE HIGH LEVEL DOMAIN EXHIBITS A SHARP ROSTRAL EDGE COINCIDENT WITH THE R4/R5 BOUNDARY AND A DIFFUSE CAUDAL EDGE LOCATED MIDWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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D77AE07AED9C2AD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; Repressor; DNA-binding; Nuclear protein. DNA BIND 238 264 BASIC MOTIF.

LEUCINE-ZIPPER.
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28-FEB-2003 (Rel. 41, Last annotation update)
Transcription factor MafB (V-maf musculoaponeurotic fibrosarcoma oncogene homolog B) (Transcription factor MAFI).
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STRAIN-Wistar; TISSUE-Liver;
MEDLINE=91190228; PubMed=903833;
Sakai M., Imaki J., Yoshida K., Ogata A., Matsushima-Hibaya Y.,
Kuboki Y., Nishizawa M., Nishi S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Pred. No. 43;
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POLY-HIS.
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01-0CT-1996 (Rel. 34, Last seq
28-FEB-2003 (Rel. 41, Last ann
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MAPB RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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spinal cord.";
Oncogene 14:745-750(1997).
-!- FUNCTION: Plays a pivotal role in regulating lineage-specific
hematopoiesis by repressing ETS1-mediated transcription of
erythroid-specific genes in myeloid cells (By similarity).
-!- SUBCELDUAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the bZIP family. Maf subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; Repressor; DNA-binding; Nuclear protein.
DNA_BIND 238 264 BASIC MOTIF.
DOMAIN 266 287 LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE=20193820; PubMed=10729156;
Afonso C.L., Tulman B.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
The genome of fowlpox virus.";
J. Virol. 74:3815-3831(2000).
-!- SIMILARITY: Belongs to the poxviruses A16 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35792 MW; 6E386340D1F840A5 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Pred. No. 43;
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PROSITE; PS50217; BZIP; 1.
PROSITE; PS00036; BZIP_BASIC; FALSE_NEG
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POLY-HIS.
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InterPro; IPR008917; Euk transcr_DNA.
InterPro; IPR004827; TF_EZIP.
InterPro; IPR004826; TF_Maf.
Pfam; PF03131; bZIP_Maf. 1.
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75.0%;
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Best Local Similarity 75.0.
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email to license@isb-sib.ch)
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MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Badcock K., Basham D., Elwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L.,
Cliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Sulston J.E., Taylor K., Whitehead S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Putative fatty-acid--CoA ligase fadD21 (EC 6.2.1.-) (Acyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773, 1765;
                                                           DB 1; Length 369;
50;
                                                                                                  Indels
                         369 AA; 42081 MW; 380A71032C18BB99 CRC64;
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                                                                                                2; Mismatches
                                                             62.5%; Score 35; 50.0%; Pred. No. E
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                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis, and Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence.";
Nature 393:537-544(1998).
         Pfam; PF03003; DUF230; 1.
                                                                                 Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                          STANDARD;
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InterPro; IPR000873; AMP-bind.
Pfam, PF00501; AMP-binding; 1.
PROSTIE; PS00455; AMP BINDING; FALSE NEG.
Hypothetical protein; Ligase; Fatty acid metabolism;
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EMBL, AL010186; CAA15862.1; -. EMBL, AE00699; AAK45479.1; -. EMBL; BX248338; CAD94078.1; -.
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Matches 7; Conservative
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ne : 5.54545 secs
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IAVPLSVP 95
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TIGR; MT1222; -
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Q99743 drosophila Q91949 oryza sativ Q9444 drosophila Q9475 oryza sativ Q9444 drosophila Q9475 oryza sativ Q9681 trypanosoma Q7125 rhodopirell Ol464 homo sapien Q9526 lactococcus Q9566 lactococcus Q9566 lactococcus Q9476 oryza sativ Q9hwv6 pseudomonas Q9429 oryza sativ Q98210 mus musculu Q98210 mus musculu Q98111 musculu Q98111 mus musculu Q98121 mus musculu Q98121 mus musculu Q98121 mus musculu Q9821 mus musculu Q98251 homo sapien Q9425 homo sapien Q9bzis homo sapien Q9825 homo sapien Q8825 homo sapien S8825 h

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Q9V743 Q9LGY9 Q9VA44 Q9AX75 Q9N8V1 Q7URU5 Q14634 Q63318 Q9CG60

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September 5, 2004, 09:46:09; Search time 22.6263 Seconds (without alignments) 139.448 Million cell updates/sec
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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1: Sp archea:*
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7: Sp_manmal:*
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ALIGNMENTS

Q870B4 Q8N218 Q9BZI4 Q9NB94 Q9BZI5

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	0914v0 atrentomyce	09s556 neemdomonas	Oga564 naeudomonae	Ognom xvlella fas	O89893 himan harna	OStone saccharomy	OBIBIO arabidonais	O89d16 bradyrbiach	O88srl lactobacill	Ogmoss bacterionba	Ognava wylella fas	OBbwa6 mis misculu	OBn7t2 homo garien	ORdmps symbologo	OB7×n8 needdomonae	Q92rn5 rhizobium m
SUMMARIES	ΠD	091440	098556	5 098564	5 Q9PBM2	2 089893	OSTGP8				0			0	OBDMPS	5 087XN8	S Q92RN5
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RESULT 2

RESULT Q9L4Y0	RESULT 1 2914Y0	
95	Q9L4YO PRELIMINARY; PRT; 109 AA.	
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S	втин.	
SO	Streptomyces olivaceus.	
ပ္ပ	Bacteria; Actinobacteria: Actinobacteridae: Actinomycerales.	
ပ္ပ	Streptomycineae; Streptomycetaceae; Streptomyces	
ŏ	NCBI_TaxID=47716;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Tu 2353;	
RX	MEDLINE=21225632; PubMed=11325225;	
RA	Rafanan E.R. Jr., Le L., Zhao L., Decker H., Shen R.	
RT	"Cloning, sequencing, and heterologous expression of the elmcHT, genes	
RI	involved in the biosynthesis of the polyketide antibiotic elloramycin	
RI	from Streptomyces olivaceus Tu2353.";	
RL	J. Nat. Prod. 64:444-449 (2001).	
DR	EMBL; AF263463; AAF73051.1;	
DR	GO; GO:0004497; F:monooxygenase activity: IRA	
DR	InterPro; IPR007138; ABM.	
DR	Pfam; PF03992; ABM; 1.	
ΚW	Monooxygenase	
Š	SEQUENCE 109 AA; 12304 MW; E65F4010C7D4B30B CRC64;	
ą,	71.48;	
M A	best Local Similarity 77.8%; Pred. No. 7.3; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps	. 0
δ	2 ISVPLSVPC 10	
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                      MEDLINE=20521925; PubMed=11069649;
Nakayama K., Takashima K., Ishihara H., Shinomiya T., Kageyama M.,
Kanaya S., Ohnishi M., Murata T., Mori H., Hayashi T.;
Kanaya S., Ohnishi M., Murata T., Mori H., Hayashi T.;
"The R-type pyocin of Pseudomonas aeruginosa is related to P2 phage, and the F-type is related to lambda phage.";
Mol. Microbiol. 38-213-231(2000).
BMBL, AB030826; BAA83139-1; -.
InterPro; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR_IPOPROTEIN; 1.
SEQUENCE 85 AA, 9252 MW; 472269231FCCG355 CRC64;
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STRAIN=ATCC 15692 / FAO1;
Nakayama K., Takashima K., Ishihara H., Shinomiya T., Kageyama M.,
Kanaya S., Ohnishi M., Murat T., Terawaki Y., Mori H., Hayashi T.;
"Genetic relationship between bacteriochns and bacteriophages.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                               Last annotation update)
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                                                                                                                                                                                                                                                                                                                         Score 39; DB 2;
Pred. No. 8.8;
            85 AA.
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                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein.
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MEDLINE-2016-17; Pubmed=10910347;

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A lavarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
A lavarenga R.H., Bonaccoreis E.D., Bordin S., Bove D.M., Estrones M.R.S.,
Buenco M.R.P., Camarco A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M.,
Coutinho L.L., Cristofani M., Dias-Neto E. Docena C., El-Dorry H.,
Radenos E.C., Franco M.C., Frohme M., Furlan L.R.,
Radenos E.C., Franco M.C., Frohme M., Furlan L.R.,
A Krieger J.S., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
A Machado M.A., Madeira A.M.B., Madeira H.M.F., Matsukuma A.Y.,
A Machado M.A., Madeira A.M.B., Madeira H.M.F., Matsukuma A.Y.,
A Machado M.A., Madeira A.M.B., Matrino E.M.F., Matsukuma A.Y.,
A Machado M.A., Madeira A.M.B., Matrino E.M.F., Matsukuma A.Y.,
A Machado M.A., Madeira A.M.B., Matrino E.M.F., Matsukuma A.Y.,
A Mani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A de Oliveira M.C., de Oliveira R.C., Pannieri D.A., Paris A.,
A de Rosa V.B. Ur., G.B., Pereira H.M. Jr., Pesquero J.B.,
A de Souza A.B., Pereira G.G., Rodrigues V., de Rosa A.J.M.,
A de Souza A.B., Terenzi M.L.Z., Siqueira W.J., de Souza A.A.,
A de Souza A.P., Terenzi M.F., Trai S.N., Tsulako M.H.,
A Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
HThe genome sequence of the plant pathogen Xylella fastidiosa.";
HThe genome sequence of the plant pathogen Xylella fastidiosa.";
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Xanthomonadaceae; Xylella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 16; Length 85;
Pred. No. 8.8;
2; Mismatches 1; Indels
"Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
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148 AA; 15990 MW; B78D2FAB6B929260 CRC64;
                                                                                                                EMBL; AB030825; BAA83170.1; -.
EMBL; AB045308; BAA9749.1; -.
EMBL; AB04498; AAG04020.1; -.
EMBL; AE00498; AAG04020.1; -.
InterPro; IPR000437; Prok lipoprot S.
PROSTITE; PS00013; PROKR LIPOPROTEIN; 1.
Hypochetical protein; Complete proteome:
SEQUENCE 85 AA; 9222 MM; F2267D9C5427748 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
10-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Xf2118.
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EMBL; AE004026; AAF84917.1; -.
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SEQUENCE
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MEDLINE=9133307; PubMed=1651403;
Teo I.A., Griffin B.E., Jones M.D.;
"Characterization of the DNA polymerase gene of human herpesvirus 6.";
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Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
"The DNA sequence of human herpesvirus-6: structure, coding content,
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human herpesvirus 6 is closely related to human cytomegalovirus.";
J. Virol. 64:287-299(1990),
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Thomson B.J., Efstathiou S., Honess R.W.;
"Acquisition of the human adeno-associated virus type-2 rep gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90080132; PubMed=2152817;
Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
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     Indels
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MEDLINE=92333249; PubMed=1321206;
Efstathiou S., Lawrence G.L., Brown C.M., Barrell B.G.;
                                                                                                                                                                                                                                                                                                        no RNA stage; Herpesviridae;
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Last annotation update)
   2,
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 Mismatches
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MEDLINE=91237802; PubMed=1851860;
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Nature 351:78-80(1991).
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Virology 209:29-51(1995).
5; Conservative
                                                                                                                                                            PRELIMINARY;
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                                 CISVPLSVPC 10
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DR2.
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Matches
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Thomson B.J., Honess R.W.; "The right end of the unique region of the genome of human herpesvirus to 1102 contains a candidate immediate early gene enhancer and a homologue of the human cyromegal.ovirus US22 gene family."; J. Gen. Virol. 73:1649-1660(1992).
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Liu D.X., Gompels U.A., Nicholas J., Lelliott C.;
"Identification and expression of the human herpesvirus 6 glycoprotein
H and interaction with an accessory 40K glycoprotein.";
J. Gen. Virol. 74:1847-1857(1993).
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                                                                                                                                                                                                                                      Geng Y., Chandran B., Josephs S.F., Wood C., "Identification and characterization of a human herpesvirus 6 gene segment that trans activates the human immunodeficiency virus type 1
"Identification of homologues to the human cytomegalovirus US22 gene family in human herpesvirus 6."; J. Gen. Virol. 73:1661-1671(1992).
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MEDLINE=93091236; PubMed=1333836;
Gompels U.A., Carss A.L., Sun N., Arrand J.R.;
"Infectivity determinants encoded in a conserved gene block of human
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MEDLINE=9402558; PubMed=7692666;
Liu D.K., Gompels U.A., Foa-Tomasi L., Campadelli-Fiume G.;
Liu n.K., Gompels U.A., Foa-Tomasi L., Campadelli-Fiume G.;
"Human herpesvirus-6 glycoprotein H and L homologs are components of the gpl00 complex and the gH external domain is the target for neutralizing monoclonal antibodies.";
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"Gene for the major antigenic structural protein (p100) of human
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Fleckenstein B.;
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J. Gen. Virol. 74:495-500(1993).
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MEDLINE=92260671; PubMed=1374813;
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MEDLINE=93187613; PubMed=8383182;
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RESULT 6

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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
11-0CT-2003 (TrEMBLrel. 25, Last annotation update)
11-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=21624570; PubMed=11753363;

MEDLINE=21624570; PubMed=11753363;

Minar A., Harrison P.M., Cheung K.H., Lan N., Echols N., Bertone I.

Miller P., Gerstein M.B., Snqder M.;

"An integrated approach for finding overlooked genes in yeast.";

"An integrated approach for finding overlooked genes in yeast.";

Nat. Biotechnol. 20:58-63(2002).

Hypothetical protein.

EKPOTHETICAL PROTECTION ALT9253.1;

EKPOTHETICAL PROTECTION ALT9253.1;

EKPOTHETICAL PROTECTION ALT9253.1;

EKPOTHETICAL PROTECTION ALT9253.1;
                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome annotation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 144;
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EMBL, AY088810; AAM67120.1;
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0003818; F:IMP dehydrogenase activity; IEA.
InterPro; IPR03009; FMN enzyme.
InterPro; IPR001093; IMPDh/GMRRtase.
InterPro; IPR001099; IMPDh/GMRRtase.
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TIGREAMS; TIGNO1302; IMP dehydrog; I.
SROGHTE; PSO0487; IMP DH GMP RED; I.
SEQUENCE 503 AA; 54218 MW; 99D478F48F4E649C CRC64;
                                                                                           Last sequence update)
Last annotation update)
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                            144 AA.
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Best Local Similarity 75.0°
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                                                                                                                                        Hypothetical protein.
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MEDILINE=93331/10; PubMed=7687803;
Pellett P., Sanchez-Martinez D., Dominguez G., Black J.B., Anton E., Greenamoyer C., Dambaugh T.R.;
A strongly immunoreactive view protein of human herpesvirus 6 variant B strain Z29: identification and characterization of the gene and mapping of a variant-specific monoclonal antibody reactive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dewhurst S., Dollard S.C., Pellett P.E., Dambaugh T.R.; "Identification of a lytic-phase origin of DNA replication in human herpesvirus 6B strain Z29."; J. Virol. 67:7680-7683(1993).
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Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z.,
Frenkel N., Rosenthal L.J.;
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pping of the
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"Characterization of human telomeric repeat sequences from human
"Characterization of numan telomeric repeat
"Herpesvirus 6 and relationship to replication.";
"Gen. Virol. 76:451-458(1995).
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Pfeiffer B., Berneman Z.N., Neipel F., Chang C.K., Tirwatnapong
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J. Virol. 68:2978-2985(1994)
                                                                                                                                                                    Virology 195:521-531(1993).
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Best Local Similarity 77.8
Matches 7; Conservative
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Gilakjan Z.A., Kropinski A.M., "Cloning and analysis of the capsid morphogenesis genes of Pseudomonas aeruginosa bacteriophage D3: another example of protein chain mail?"; J. Bacteriol. 181:7221-7227(1999).
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
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     GO; GO:0000034; F:adenine deaminase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR06680; Amidohydro_1.
Pfam; PF01979; Amidohydro_1; 1.
Hydrolase; Complete proteome.
SEQUENCE 563 AA; 60927 MW; A4B5159C11718FA7 CRC64;
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J. Bacteriol. 182:606-6074 (2000).
EMBL, AF165214; AAF80793.1;
InterPro. 157000137; Prok lipoprot S. PROSITE; PS000137; PROKIL LIPOPROTEÏN; 1.
SEQUENCE 86 AA; 9389 Mw; 86ABCABS2A9E5
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watenabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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MEDLINE=22480296; PubMed=1256566;
Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Klaperso O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing Be Vos W.M., Siezen R.J.;
"Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; APO65962; BAC52894.1; -.
InterPro; IPR002830; carboxylyase.
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Bradyrhizobiaceae; Bradyrhizobium.
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PROSITE; PS00024; HEMOPEXIN; 1.
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284 CLTVPLEVP 292
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82 VSVPLSVP 89
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 SEQUENCE FROM N. A. S. STRUBLAGE, MEDLINE=22354683; PubMed=12466851; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium, The PANTOM Consortium, The RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).

EMBL; AK053082; BAC35260.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical sugar phosphatases structure containing protein.
Mus muscula (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

66.1%; Score 37; DB 11; Length 129;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                    Score 37; DB 16; Length 89; Pred. No. 22;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 129 AA; 13584 MW; DOB83B75AFAD595B CRC64;
                                                                                                                                                                                                                               Hypothetical protein; Complete proteome.
SEQUENCE 89 AA; 9641 MW; F13175F1054D6130 CRC64;
                                                                                                                                                                                                                                                                                                                                     129 AA.
                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                      PRT;
MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                    66.1%;
66.7%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                           Illourand A. Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

BMBL; AK097701; BAC05145.1; -.
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                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto & Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Mareuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1."; pnA Res. 9:123-130(2002).

EMBL; AP065369; BAC07619.1; -. Complete proteome.

SEQUENCE 155 AA; 17833 MW; 16CEF9F696CEC331 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.1%; Score 37; DB 4; Length 134; 60.0%; Pred. No. 32;
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Bacteria; Cyanobacteria; Chrococccales; Synechococcus.
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Last annotation update)
                                                                     01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothelical protein FLJ40382.
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Pred. No. 37;
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  134 AA
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MEDLINE=22225144; PubMed=12240834;
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77.8%;
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Best Local Similarity 77.0.
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                                                                                                                                                     Homo sapiens (Human).
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46 CIAGPLLLPC
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NCBI_TaxID=32046;
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Search completed: September 5, 2004, 10:00:07 Job time: 24.6263 secs

1 CISVPLSV 8 |:|:|||: 39 CVSIPLSI 46

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(c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

5, 2004, 09:37:49; Search time 32.8283 Seconds (without alignments) 86.068 Million cell updates/sec September е :: Run

US-09-761-636A-13

CISVPLSVPC 10 score: Sequence: Perfect

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

geneseqp1980s:\*
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geneseqp2000s:\*
geneseqp2001s:\* A Geneseq 29Jan04:\* 1: geneseqp1980s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aau04532 VEGF base	6 VEGF	Human		3 VEGF	5 VEGF	4 VEGF	Humar	Human	Human	Нишап	VEGF b							Arabid			Abb15040 Human ner			Droso
SUMMARIES	ID	AAU04532	AAU04526	AAR66394	AAU04542	AAU04533	AAU04545	AAU04544	AAM95534	ABB96216	AAM95827	ABB96358	AAU04543	ABG12542	ABG12530	AAM16003	ABB20407	ABG37710	ADB64084	AAG30888	AAG20989	AAG43108	ABB15040	ABB67498	ABG21894	ABB65635
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%	Query	100.0	81.2	80.4	77.7	74.1	74.1	72.3	9.69	9.69	9.69	9.69	68.89	67.9	67.9	67.9	67.9	6.79	67.9	67.9	7.	7.	66.1		66.1	66.1
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	Abg71244 Guinea pi Aar96138 Profease		Aaw46562 Peptide b	Aau58478 Propionib	Abm54997 Propionib	Abp64007 Human ORF	Aab45459 Human sec	Aab45460 Human sec	Aaq89148 Human sec	Нишап		Abg19452 Novel hum	Aau66053 Propionib	Abm62572 Propionib	Aaq04076 Human sec		Aam80011 Human pro	Abb54586 Lactococc
ABG20151	ABG/1244 AAR96138	AAW82212	AAW46562	AAU58478	ABM54997	ABP64007	AAB45459	AAB45460	AAG89148	AAB45461	AAB45462	ABG19452	AAU66053	ABM62572	AAG04076	AAM79027	AAM80011	ABB54586
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26	7 8 7 7 8 7	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAU04532 standard; peptide; 10 AA. VEGF based monocyclic peptide 10. entry) (first 26-SEP-2001 AAU04532; RESULT 1 AAU04532 

Human, VEGF, vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic.

 .10 /note= "This bond cyclises the peptide" Location/Qualifiers 18-JAN-2001; 2001WO-US001533 Key Disulfide-bond WO200152875-A1. 26-JUL-2001.

(LUDW-) LUDWIG INST CANCER RES. 18-JAN-2000; 2000US-0176293P.

Stacker Hughes RA, Achen MG,

Cendron A;

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WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

residues

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides and a cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis.

Co neovascularisation or lymphangiogenesis in a mammal with a condition characterised by anglogenesis, neovascularisation or lymphangiogenesis.

Co recentation is diabetic retinopathy, psoriasis, arthropathy, correbrovascular accident, post-angioplasty restenosis, heat or cold trauma, substance-induced neovascularisation of the liver, excessive cerebrovascular accident, post-angioplasty restenosis, head, heat or clauma, substance-induced neovascularisation of the liver, excessive crevelace, hypertension induced neovascular sequelace, nor chronic liver infection. The peptides are also used to modulate vascular permeability con a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to induced neovascular corrections or brain. The peptides are used to induced by VEGF, vEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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    .11
    /note= "This bond cyclises the peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                               diabetic retinopathy
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Best Local Similarity
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human upon visit of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a petide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior peptides) and a cyclic peptide with at least one amino acid deleted prior correlation are used to interfere with angiogenesis.

CC cyclisation are used to interfere with angiogenesis.

CC cyclisation are used to interfere with angiogenesis.

CC changing, wascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or crauma, substance-induced neovascularisation of the liver excessive corpuspone related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability corpusation in peripheral limbs or in lungs, peritoneal cavity, pleura, accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic with at least one biological activity induced by VEGF C or D and are also used in combination with an anti-inflammatory agent, to treat a chrimmation inflammation with an anti-inflammatory agent, to treat a chrimmation related to relate the manner of the control of are also used in combination with an anti-inflammatory agent, to treat a chrimmatory related to relate the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1,
                                                                                                                                   sequence represents a monomeric monocyclic peptide of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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    .141
    /note= "X corresp. to translated stop codon"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45.5; DB
Pred. No. 0.56;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Friedhoff AJ, Basham DA, Miller JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR66394 standard; peptide; 141 AA.
                                                                       Claim 49; Page 32; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-US005445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.2%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Psychosis protecting peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-00060560.
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(first entry)
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Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CISVPL-SVPC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetic retinopathy
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11-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU04542 standard; peptide; 11 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEGF based monocyclic peptide 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 CISIPLSIP 36
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                              WPI; 1995-006234/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-442248/47.
                                                      N-PSDB; AAQ75090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200152875-A1
                                                                                                                                                                          schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU04542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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ANU04542
DAVO04542
DAVO04542
DDT 26-5
DDT 26-6
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New nucleic acids encoding psychosis protecting peptide and antibodies - for the treatment, diagnosis and research of psychotic disorders, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.4%; Score 45; DB 2
77.8%; Pred. No. 9.4;
iive 2; Mismatches
                                                                                                                                                                                    Claim 1; Page 56; 87pp; English
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whose 3-dimensional structure is modelled on the expose loop of human CGFPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and confidence of peptide by oxidising the existence residues. The monocyclic peptides by oxidising the expense (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior peptides) and a cyclic peptide with at least one amino acid deleted prior corpitation are used to interfere with angiogenesis, neovacularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, heat or cold trauma, substance induced neovascularisation of the liver excessive

sequence represents a monomeric monocyclic peptide of the invention,

Example 25; Page 47; 102pp; English.

hormone-related angiogenic dysfunction, diabetes induced necvascular sequelae, hypertension induced necvascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. Or -D and are also used in combination with an anti-inflammatory agent, to treat a

inflammation, especially rheumatoid arthritis, psoriasis and

diabetic retinopathy

chronic

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ij,
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                   Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                           neovascularisation, lymphangiogenesis, psoriasis, tumour, diabetes induced neovascular sequelae; rheumatoid arthritis, diabetic retinopathy, chronic inflammation, cyclic.
                                                                                                                                                                                                                                                        4; Length 11;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                      Score 43.5; DB
Pred, No. 1.2;
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     VEGF based monocyclic peptide 11.
                                                                                                                                                                                                                                                                                                                                        AAU04533 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0176293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                      77.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                     26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                    1 CISVPL-SVPC 10
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1 CLSVPLTSVPC 11
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                        Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                       AAU04533;
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                AAU04533
ID AAU0
XX
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(LUDW-) LUDWIG INST CANCER RES

Cendron A;

Cendron A;

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AAU04545 standard; peptide; 11 AA.
                                         Claim 49; Page 32; 102pp; English.
                                                                                                                                                                                                                                                       VEGF based monocyclic peptide 23.
                                                                                                                                                                                                                                               26-SEP-2001 (first entry)
                                                                                                                                                                           Ouery Match
Best Local Similarity 90.0.
Local 9; Conservative
                                                                                                                                                                                                1 CISVPLSVPC 10
    Achen MG, Hughes RA,
                                                                                                                                                                diabetic retinopathy
            WPI; 2001-442248/47.
                                                                                                                                                                                                      CISVPL-VPC
                                                                                                                                                                       Sequence 9 AA;
                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                       AAU04545;
                                 residues.
                                                                                                                                                                                                                      RESULT 6
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whose 3-dimensional structure is modelled on the expose loop of human vEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betacarbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cycliding the peptide by oxidishing the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis, or neovascularisation or lymphanglogenesis in a mammal with a condition characterised by anglogenesis, neovascularisation or lymphanglogenesis, recovacularised and a cyclic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angloplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive
                                                                                                                                                                                                                                                                                                                                                                                                 Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. VEGF-C or -D and are also used in combination with a anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a monomeric monocyclic peptide of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.1%; Score 41.5; DB 72.7%; Pred. No. 2.5; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU04544 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                      Stacker S,
                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES
                                                                               18-JAN-2001; 2001WO-US001533.
                                                                                                                                      18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                         Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                             WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11 AA;
                        26-JUL-2001
                                                                                                                                                                                                                                                                                         Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                residues.
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                                                                                                                                                                                                                                                                                                                                       The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vegety (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabet a carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis archropathy, characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis arthropathy, the meangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                         Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic with at least one biological activity induced by VEGF. Or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neovascularisation, lymphangiogenesis, psoriasis, tumour;
diabetes induced neovascular sequelae, rheumatoid arthritis;
diabetic retinopathy, chronic inflammation, cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41.5; DB 4; Length 9;
Pred. No. 1.4e+06;
0; Mismatches 0; Indels
                              Cendron A;
                              Stacker S,
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90.0%;
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ij

Gaps

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5

4; Length 11; Indels Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation, lymphangiogenesis, psoriasis, tumour; diabetes induced neovascular sequelae, rheumatoid arthritis;

/note= "This bond cyclises the peptide"

Location/Qualifiers

Digulfide-bond

WO200152875-A1

VEGF based monocyclic peptide 22.

(first entry)

26-SEP-2001

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21-NOV-2001 (first entry)
                                                                                                                                            cancer; gene therapy
                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2000;
                                                                                                                                                                                                                                                                02-AUG-2001.
    AAM95534;
    The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human verges (vascular endchelal growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betace the carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cystein residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

Co cyclisation are used to interfere with angiogenesis.

Co cyclisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

Co cyclisation is diabeted retrinopathy, psoriasis, arthropathy, cerebrovascular accident, post-arinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive contenums, substance-induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limps or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by WEGF or D and are also used in combination with an anti-inflammatory agent, to treat a continion inflammation, especially rheumatoid arthritis, peritors and alphanation with an anti-inflammatory agent, to treat a continion related and and activity induced by Vescoriasis and alphanatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.3%; Score 40.5; DB 4; Length 11; 72.7%; Pred. No. 3.7; ive 2; Mismatches 0; Indels
                                                                                                                   /note= "This bond cyclises the peptide"
diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                     Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 25; Page 47; 102pp; English.
                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     Achen MG, Hughes RA, Stacker S,
                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                         18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                 18-JAN-2000; 2000US-0176293P
16-MAY-2000; 2000US-0204590P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CISVPL-SVPC 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11 AA;
                                                                                                Disulfide-bond
                                                                                                                                                             WO200152875-A1
                                                                                                                                                                                                   26-JUL-2001
                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel
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AAM95534
ID AAM9
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AAM95534 standard; protein; 77 AA.

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Human; reproductive system related antigen; reproductive system disorder;
Human reproductive system related antigen SEQ ID NO: 4192.
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2000US - 0217486P

2000US - 021890P

2000US - 0220964P

2000US - 0224519P

2000US - 0225114P

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2000US - 022514P

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2000US - 0225214P

2000US - 022527P

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2000US-0190076P.
2000US-0198123P.
2000US-0209467P.
2000US-0214886P.
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2000US-0226868P.
2000US-0227182P.
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2000US-0229345P.
2000US-0229509P.
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2000US-0186350P.
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2000US-0234223P.
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2000US-0249212P.
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2000US-0249244P.
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2000US-0236370P.
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2000US-0246524P
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                                                  14-8EP-2000;
21-8EP-2000;
25-8EP-2000;
25-8EP-2000;
25-8EP-2000;
27-8EP-2000;
27-8EP-2000;
27-8EP-2000;
29-8EP-2000;
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Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic.
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                                                                                                                                                                                                                                                           Claim 11; SEQ ID NO 4192; 1297pp + Sequence Listing; English.
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08-DEC-2000; 2000US-0251856P.

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11-DEC-2000; 2000US-0251997P.
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2000US-0215135P.
2000US-021647P.
2000US-021647P.
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Best Local Similarity 40.0
Matches 4; Conservative
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CLNAPIRIPC 56
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24-FBB-2000, 2
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119-MAY-2000, 2
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111-JUL-2000) 2000US-0218290P.
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HUMA-) HUMAN GENOME SCI Barash SC, Rosen CA,

WPI; 2001-483232/52

Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.

Claim 11; SEQ ID NO 1600; 766pp; English

The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a protein of the invention

Sequence 77 AA;

Score 39; DB 4; Length 77; Pred, No. 48; 69.68; Query Match Best Local Similarity

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    Gaps
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Pred. No. 68;
1; Mismatches
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04-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0184664P.
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Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
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17-NOV-2000;
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                                                                                                       08-NOV-2000;
08-NOV-2000;
                                                                                                                        08-NOV-2000;
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05-DEC-2000;
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGED (vascular endothellal growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising comprising 2 linked monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphandiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                 sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a protein of the
numan testicular antigens, and fragments of their genomic sequences. The
                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; VEGF; vascular endothelial growth factor; anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neovascularisation, lymphangiogenesis, psoriasis, tumour; diabetes induced neovascular sequelae, rheumatoid arthritis, diabetic retinopathy, chronic inflammation, cyclic.
                                                                                                                                                                      Length 108;
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "This bond cyclises the peptide"
                                                                                                                                                                    Query Match 69.6%; Score 39; DB 4;
Best Local Similarity 77.8%; Pred. No. 68;
Matches 7; Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stacker S,
                                                                                                                                                                                                                                                                                                                                                                               AAU04543 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGF based monocyclic peptide 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hughes RA,
                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                                                                 2 ISVPLSVPC 10
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                                                                                                                                                                                                                                                                        33 VSVPLSHPC
                                                                                                                                  Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200152875-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residues.
                                                                                                invention
                                                                                                                                                                                                                                                                                                                                                                                                                     AAU04543;
                                                                                                                                                                                                                                                                                                                                              RESULT 12
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The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery corecebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver confection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid coremination in peripheral limbs or in lungs, peritoneal cavity, pleura, core brain. The peptides are used to image blood vessels and lymphatic core brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VBGF, VBGF-C or D and care also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and characterials and chronic arthritis, psoriasis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                             Score 38.5; DB 4; Length 11; Pred. No. 7.8; 0; Indels 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 42901; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #12533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG12542 standard; protein; 59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YT,
                                                                                                                                                                                                                                                                                                                                                                   68.8%;
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2000US-00649167
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CISVPL-SVPC 10
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CITIPLISLPC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS76729
                                                                                                                                                                                                                                                                                                                          Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000;
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              Supplement. (II) and its binding partrers are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
 polypeptide in tissue, as molecular weight markers and as a food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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0
                                                                                                                                                                                                                                                                                     4; Length 59;
                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                 67.9%; Score 38; DB 70.0%; Pred. No. 53; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 42889; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #12521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG12530 standard; protein; 59 AA.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                      Local Similarity 70.0
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                            1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                          CISVLVPVPC
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N-PSDB; AAS76717.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                    Sequence 59 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-2002
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the invipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #2437 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; human; microarray; gene expression; cervical epithelial cell;
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                                                                                                                                                                                                                                     DB 4; Length 59;
53;
                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                        1; Mismatches
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                                                                                                                                                                                                                                     Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                     AAM16003 standard; protein; 71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                                                                                     67.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                     1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                          9 CISVLVPVPC 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488901/53
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cervical cancer.
                                                                                                                                                                                                      Sequence 59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
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                                                                                                                                                                                                                                                                      Matches
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                                        Gaps
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                   DB 4; Length 71;
65;
                                        2; Indels
                                        Mismatches
                                                                                                               Search completed: September 5, 2004, 09:55:21 Job time : 34.8283 secs
                    Score 38;
Pred. No. 6
                                        .
                    67.98;
                                         Conservative
                                                                                51 CISVPLPTP 59
                                                             Q
         Query Match
Best Local Similarity
7, Conserve
                                                           1 CISVPLSVP
Sequence 71 AA;
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100.0%; Score 56; DB 9; Length 10; llarity 100.0%; Pred. No. 0.023; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-761-636A-7
; Sequence 7, Application US/09761636A
; Patent No. US20020065218A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CISVPLSVPC 10
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-09-761-636A-13
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35.5
35.5
Sequence 4192, Ap
Sequence 58210, A
Sequence 4485, Ap
Sequence 50298, A
Sequence 24, Appl
Sequence 35705, A
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Sequence 23, Appli
Sequence 174203,
Sequence 14, Appl
Sequence 26, Appl
Sequence 264847,
Sequence 25, Appl
Sequence 25, Appl
                                                                                               September 5, 2004, 10:00:15 ; Search time 28.0808 Seconds
(without alignments)
112.199 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/NEG_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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9 US-09-761-636A-23

16 US-09-761-636A-23

19 US-09-761-636A-14

10 US-09-761-636A-26

12 US-09-761-636A-26

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13 US-09-761-636A-26

14 US-10-45-59-264847

15 US-10-437-963-167-987

16 US-10-425-114-58210

17 US-10-425-114-58210

18 US-10-425-114-50298

19 US-09-764-891-4485

10 US-09-764-891-4485

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10 US-09-764-891-485

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Maximum Match 1008
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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1 CISVPLSVPC 10
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Match Length DB
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Sequence 140110,
Sequence 2238, Ap
Sequence 7910, Ap
Sequence 7911, Ap
Sequence 17912, Ap
Sequence 125857,
Sequence 125857,
Sequence 6, Appli
Sequence 228957,
Sequence 28991,
Sequence 28991,
Sequence 28991,
                                                                                                                                                                                                                                                                                   Sequence 754, App
Sequence 29825, A
Sequence 268, App
Sequence 268, App
Sequence 10647,
Sequence 184465,
Sequence 2, Appli
Sequence 198582,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3554, Ap
Sequence 60080, A
Sequence 7446, Ap
Sequence 7, Appli
Sequence 119123,
Sequence 576, App
Sequence 576, App
Sequence 576, App
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SQUENCE 13, Application US/09761636A

SQUENCE 13, Application US/09761636A

GENERAL INFORMATION:

APPLICANT: STACKER, Steven

APPLICANT: GTORN, Angela

APPLICANT: HUGHES, Richard

APPLICANT: CENDRON, Angela

TITLE OF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT PILLON NUMBER: US/09/761,636A

CURRENT FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR PLICATION NUMBER: US 60/176,293

PRIOR PLICATION NUMBER: US 60/204,590

PRIOR PLICATION NUMBER: US 60/204,590

SPRIOR PLING DATE: 2000-01-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.0

SEQ ID NO 13

LENGTH: 10
2 US-10-424-599-220123

6 US-10-104-047-293

5 US-10-134-047-293

6 US-10-135-977-7910

2 US-10-335-977-7911

2 US-10-335-977-7911

2 US-10-335-977-7911

2 US-10-335-977-7911

2 US-10-437-963-125857

6 US-10-437-963-125857

6 US-10-437-963-125857

8 US-10-087-110-6

3 US-10-437-963-199587

US-10-424-599-2886

0 US-09-386-259825

4 US-10-087-1963-199587

0 US-10-424-599-198582

2 US-10-424-599-198582

2 US-10-424-599-198682

2 US-10-425-114-60080

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5 US-10-425-114-60080

6 US-09-852-7

6 US-09-915-576
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ORGANISM: Homo sapiens

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Gaps

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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 174203
LENGTH: 140
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Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: APPLICANT: STACKER, Steven

APPLICANT: STACKER, Steven

APPLICANT: CENDROW, Angle

TITLE OF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US/09/761,636A

CURRENT FILING DATE: 2000-01-18

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SEQ ID NOS: 34

SEQ ID NO 14

FENDRAL PATENTING OF SEQ ID NOS: 34

SEQ ID NO 14

FENDRAL PATENTING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 14

FENDRAL PATENTING DATE: 2000-05-16

SEQ ID NO 14

FENDRAL PATENTING DATE: 2000-05-16

SEQ ID NOS: 34

FENDRAL PATENTING DATE: 2000-05-16

FENDRAL P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
COTHER INFORMATION: Clone ID: PAT_MRT4530_72167C.1.pep US-10-437-963-174203
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LOCATION: (1)..(140)
OTHER INFORMATION: unsure at all Xaa locations
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Patent No. US20020065218A1
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
    Boukharov, Andrey A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                Barbazuk, Brad
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Matches 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
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ORGANISM: Homo sapiens
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US-09-761-636A-26
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APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: BY ACKER, Steven
APPLICANT: HUGHES, Nobela
APPLICANT: HUGHES, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VESSION 3.0
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Pred. No. 2.3;
1; Mismatches 0; Indels
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PUblication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 81.2%;
Best Local Similarity 90.9%;
Matches 10; Conservative (
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US-09-761-636A-23
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Best Local Similarity 81.8%;
Matches 9; Conservative
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ORGANISM: Homo sapiens
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US-09-761-636A-23
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Sequence 167987, Application US/10437963
Publication No. US20040123343A1
GENERAL INPORMATION:
PAPLICANT: La Rosa, Thomas J.
APPLICANT: Each, Vihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4192
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 11;
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Publication No. US20030077803A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PCOO6
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 40.5; DB 9;
Pred. No. 6.7;
2; Mismatches 0;
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LOCATION: (1)..(279)
OTHER INFORMATION: unsure at all Xaa locations
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 167987
LENGTH: 279
            PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                              72.3%;
72.7%;
                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-25
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Best Local Similarity 77.8
Matches 7; Conservative
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Matches 8, Conservative
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ORGANISM: Oryza sativa
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US-09-764-891-4192
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Covalic David K
APPLICANT: Cao Yongwei
APPLICANT: 
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; Patent No. US2002065218A1
; GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
; TITLE OP INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR FILING DATE: 2000-01-18
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR APPLICATION NUMBER: US 60/204,590
; RIOR APPLICATION NUMBER: US 60/204,590
; ROOFWARE: PALENTI VERSION 3.0
; SOFFWARE: PALENTIN VERSION 3.0
; SEQ ID NO 26
; LENGTH.1.1
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Pred. No. 39;
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US-10-424-599-264847
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Pred. No. 4.7;
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72.7%;
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; ORGANISM: synthetic construct
US-09-761-636A-26
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Best Local Similarity 72.7
Best Local Similarity 72.7
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Best Local Similarity 70.0
Matches 7; Conservative
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US-10-424-599-264847
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US-09-761-636A-25
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Sequence 50298 Application US/10425114

Publication No. US20040034688A1

GENERAL INCORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic, Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
FEWALT APPLICANT OF SEQ ID NOS: 73128
                                                                                                                                                                                                                            ; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-4485
                                                                        LOCATION: (51)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                         OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CRNDRON, Angela
TITLE OF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT PILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
                                                                                                                                                                                                                                                                                                                         Score 39; DB 10; Length 108; Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                         69.6%;
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Best Local Similarity 77.5
France 7; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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ORGANISM: Zea mays
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                                                      NAME/KEY: SITE
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Con Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO SR10
LENGTH: 83
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                                      FRATURE:

NAME/KEY: SITE

LOCATION: (38)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

LOCATION: (65)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-891-4192
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4485
LENGTH: 108
                                                                                                                                                                                                                                                                      Query Match 69.6%; Score 39; DB 10; Length 77; Best Local Similarity 40.0%; Pred. No. 74; Matches 4; Conservative 4; Mismatches 2; Indels
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Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
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Publication No. US20040034888A1
GENERAL INFORMATION:
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Best Local Similarity 75.v.
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47 CLNAPIRIPC 56
TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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68 TVPLSIPC 75
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US-09-764-891-4485
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Gaps

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FEATURE:
COTHER INFORMATION: MAP TO AL078621.19
COTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.91
COTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7
COTHER INFORMATION: EST HUMAN HIT: BF125501.1, EVALUE 1.70e+00
COTHER INFORMATION: SWISSPROT HIT: P11992, EVALUE 2.20e-01
US-09-864-761-35705
                                                                                                                  Score 38; DB 9; Length 71;
Pred. No. 98;
0; Mismatches 2; Indels
                                                                                                                                                                                                                          5, 2004, 10:29:23
                                                                                                                  Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                          Search completed: September
Job time: 29.0808 secs
   ORGANISM: Homo sapiens
                                                                                                                                                                 1 CISVPLSVP 9
                                                                                                                                                                                        51 CISVPLPTP
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                                                                                                         Length 11;
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                                                                                                      Query Match 68.8%; Score 38.5; DB 9;
Best Local Similarity 63.6%; Pred. No. 14;
Matches 7; Conservative 3; Mismatches 0;
                                                                                                                                                                                                                       US-09-864-761-35705

; Sequence 35705, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ.ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ.ID NO 24
LENGTH: 11
                                                         ; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-24
                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
                                                                                                                                                     1 CISVPL-SVPC 10
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| CITIPLTSLPC 11
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September Run on:

5, 2004, 09:55:30; Search time 8.88889 Seconds (without alignments) 58.079 Million cell updates/sec

US-09-761-636A-13 56 1 CISVPLSVPC 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 seqs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgm2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/PcTUS\_COMB.pep:\*
/cgm2\_6/ptodata/2/iaa/PcTUS\_COMB.pep:\* Issued Patents AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ф			SUMMARIES	
Result No.	Score	Query Match	Length	E0	ID	Description
Н		9.69	244	4	US-09-252-991A-32454	quence 3245
7		σ	306	4	-09-252-991A-231	equence 2316
е		66.1	142	4	-09-252-991A-2338	Sequence 23382, A
4		ø	154	4	-09-2	1880
ഗ		4	9	Н	-08-331-383-3	33,
9		4	6	П	-08-54	43,
7		4	σ	m	-08-802	143,
80		4	92	4	-09-252-991A-2	Sequence 29933, A
σ		4	192	4	-09-621-	5605,
10		64.3	341	4	-09-25	29740,
11		4	510	4		26663,
12	36	4	700	4	-09-252-991	Sequence 19384, A
13		62.5	183	4	-09-252-9	30161,
14	m	N	201	4	-09-198-4522	145
15	4.		72	٣	-722-7	58,
16		ä	72	4	-09-334-95	58,
17	4.	•	72	4	09-334-923A-5	58,
18	4	ä	72	4	-334	58
19		61.6	73	m	-08-722-719-2	26,
20	4	÷	73	m	-08-722-719-5	57,
21	4.	ij	73	4	-951-2	
22	4	÷	73	4	US-09-334-951-57	57,
23	4.	ä	73	4	-09-334-9	26
24	4.	i.	73	4	-09-33	57,
25	4	ä	73	4	US-09-689-693-26	26,
26	٠		73	4	-09-334-954A-2	26,
27	34.5	i.	73	4	US-09-334-954A-57	Ŋ

Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appli	Appl	Appl	App1
39		55,	55,	55,	24,		59		56,					4	24,	26,	59,
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-689-693-39	US-08-722-719-55	US-09-334-951-55	US-09-334-923A-55	US-09-334-954A-55	US-08-722-719-24	US-08-722-719-56	US-08-722-719-59	US-09-334-951-24	US-09-334-951-56	US-09-334-951-59	US-09-334-923A-24	US-09-334-923A-56	US-09-334-923A-59	US-09-689-693-4	US-09-334-954A-24	US-09-334-954A-56	US-09-334-954A-59
4	c	4	4	4	n	m	m	4	4	4	4	4	4	4	4	4	4
74	75	75	75	75	94	9/	9/	9/	9/	76	26	9/	16	16	16	9/	97
9.19	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	9.19	61.6	9.19	61.6	9.19	61.6	61.6	61.6	9.19
34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5	34.5
28	29	30	31	32	33	34	35	36	37	38	39	40	41	12	<del>1</del> 3	14	5

## ALIGNMENTS

JS-09-252-991A-32454

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GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 107196_136
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3.2454
LENGTH: 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
Sequence 32454, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Sequence 21169, Application US/09252991A
Sequence 2169, Application US/09252991A
Fatent No. 6551795
GENERAL INFORMATION:
TOTALE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23169
TYPE: PRT RESULT 2 US-09-252-991A-23169

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TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 4; Conservi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-549-008-43
                                    US-08-331-383-33
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                                                                                                                                                                                                                                                                                       APPLICATION TO SEED AND AND AND ACTOR SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107196.136
CURRENT PAPILOATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: US/0/074,788
PRIOR FILING DATE: US/0/074,788
PRIOR FILING DATE: US/0/094,190
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ADERUCANOSA FOR DIAGNOSTICS AND THERAPEUTICS.

FILE REFRENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

ENGRH FILENCES AND THE SEQ ID NOS: MARCH AND THE SEQ ID NO 18804
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Pred. No. 57;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 4; Length 142;
Pred. No. 52;
2; Mismatches 3; Indels
                                                     DB 4; Length 306; 55;
                                                                                          Indels
                                                                                          Mismatches
                                                   Score 39;
Pred. No. 5
                                                                                                                                                                                                                                      US-09-252-991A-23382
; Sequence 23382, Application US/09252991A
; Patent No. 6551795
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23169
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50.0%;
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50.0%;
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ilarity 70.0%;
Conservative C
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Best Local Similarity 50.v
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137 CSSLPMRLPC 146
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89 CLPPPISAPC 98
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Best Local Similarity
These 7; Conserve
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US-09-252-991A-18804
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LENGTH: 142
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Sequence 29933, Application US/09252991A

Sequence 29933, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29933

LENGTH: 92
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Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.3%; Score 36; DB 4; Length 92; 55.6%; Pred. No. 48; 1; Indels ive 3; Mismatches 1; Indels
                                                                                                                                                                     0; Indels
                                                                                                                            Length 9;
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APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5605
LENGTH: 192
                                                                                                                       Score 36; DB 3;
Pred. No. 3e+05;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa US-09-252-991A-29933
                                                                                                                            64.3%;
50.0%;
                                                                                                                                              Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 64.3
Best Local Similarity 55.6
Matches 5; Conservative
                                                             ; MOLECULE TYPE: peptide US-08-802-981-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CISVPLSVPC 10
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ORGANISM: Homo sapiens
FEATURE:
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US-09-621-976-5605
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                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-29933
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                                                                                                                            Query Match
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Sequence 143 Application US/08802981

Sequence 143 Application US/08802981

Sequence 143 Application US/08802981

Sequence 143 Application US/08802981

SERVICANT: Romoriya, Akira

APPLICANT: Romoriya, Akira

APPLICANT: Packard, Beverly S.

TITLE OF INVENTION: Compositions for the Detection of Enzyme

TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof

NUMBER OF SEQUENCES: 231

CORRESPONDENCE ADDRESS:

ADDRESSE: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California
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Pred. No. 3e+05;
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SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/549,008
FILING DATE: 27-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981 FILING DATE: 20-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTATION NUMBER: 016865-000300US
REERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                 32,762
ER: 016865-000110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                            CLASSIFICATION: 4.5.
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 016865-000
TELECHOMICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
JELEPHONE: (415) 576-0300
JELEPHONE: (415) 576-0300
JELEPHONE: 9 SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-549-008-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SVPLSVPC 10
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2 AIPMSIPC 9
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ZIP: 94111-3834
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GENERAL INCORPATION:
APPLICANT: Griffais, R.
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MAKE O. Rubenfield et al.
APPLICANT: MAKE O. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107195.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OP SEQ ID NOS: 33142
SEGO ID NO 30161
LENGTH: 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 62.5%; Score 35; DB 4; Length 183; Similarity 60.0%; Pred. No. 1.4e+02; 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.5%; Score 35; DB 4; Length 201;
; CURRENT APPLICATION NUMBER: US/09/252,991A; CURRENT FILING DATE: 1999-02-18; PRIOR APPLICATION NUMBER: US 60/074,788; PRIOR FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 19384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 30161, Application US/09252991A; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 145, Application US/09198452A
; Patent No. 6559294
                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0.
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Matches 6; Conserv
                                                                                                                                                                                                                                                           US-09-252-991A-19384
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US-09-198-452A-145
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LENGTH: 201
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                                                                                                                           GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABCUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29740
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APPLICANTON: DOUGH OF SEQUENCES AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 50/094,190
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Patent No. 6551793
BACENT NO. 6551793
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
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Pred. No. 1.98+02;
2; Indels
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                                                                                       Sequence 29740, Application US/09252991A
Patent No. 6551795
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US-00-252-991A-26663
; Sequence 26663, Application US/09252991A
; Patent No. 6551795
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illarity 60.0%;
Conservative
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 CIAVAAAIPC 368
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Best Local Similarity
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US-09-252-991A-19384
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LENGTH: 510
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Sequence 58, Application US/08722719

Patent No. 6001606

GENERAL INFORMATION:
APPLICANT: ROSEN, CRAIG A.
APPLICANT: ROSEN, TEVEN M.
APPLICANT: LI, HACDONG

TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: TREATING DISEASE STATES WITH MYELOID PROGENITOR INHIBITORY TITLE OF INVENTION: (M-CIF), AND MACROPHAGE INHIBITORY FACTOR.

TITLE OF INVENTION: (M-CIF), AND MACROPHAGE INHIBITORY FACTOR.

TITLE OF INVENTION: (M-CIF), AND MACROPHAGE INHIBITORY FACTOR.

CORRESPONDENCE ADDRESS: 64

ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRES
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                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.: 1100 NEW YORK AVENUE, N.W., SUITE 600 WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: DC
CUMNEY: USA
ZIP: 20005-3934
COMPUTER READBABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,719
FILING DATE: 30-SEP-1996
CLASSIFICATION: 435
PRICK APPLICATION NUMBER: US 08/173,209
FILING DATE: 22-DEC-1993
PRICK APPLICATION NUMBER: US 08/208,339
FILING DATE: 08-MAR-1994
PRICK APPLICATION NUMBER: US 08/446,881
FILING DATE: 08-MAR-1995
FILING DATE: 05-MAY-1995
PRICK APPLICATION NUMBER: US 08/465,682
FILING DATE: 06-UUN-1995
PRICK APPLICATION NUMBER: US 08/465,682
FILING DATE: 06-UUN-1995
PRICK APPLICATION NUMBER: US 08/465,682
FILING DATE: 06-UUN-1995
PRICK APPLICATION NUMBER: US 08/468,775
FILING DATE: 06-UUN-1995
MAND. CHEERE US 08-UN-1995
MAND. CHEERE US 08-UN-1995
MAND. CHEERE US 08-UN-1995
MAND. CHEERE US 08-UN-1995
    Pred. No. 1.6e+02;
2; Mismatches 1;
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REGISTRATION VINDRER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0330007
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2560
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
        62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                   |:|: |||
104 SIPVDVPC 111
                                                                                                                                  3 SVPLSVPC 10
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7 CISYTPRSIPC 17
1 CIS-VPLSVPC 10
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Search completed: September 5, 2004, 10:22:01 Job time : 9.88889 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 5, 2004, 09:47:29; Search time 6.90909 Seconds (without alignments) 125.302 Million cell updates/sec Run on:

US-09-761-636A-14 52 1 CISVPLVPC 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* 1 2 K 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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65.4 1876 63.5 339 63.5 370 63.5 434
സ 72 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

probable cation tr	hypothetical prote	probable dehydroge	probable dehydroge	probable ribonucle	probable DNA-direc	prestalk protein p	structural polypro	cutl protein - fis	cutl protein - fis	lon protein - Esch	ES protein - human	thrombospondin - b	probable inclusion	hypothetical prote	dual specificity p
F70757	A65072	B91098	F85943	T41246	S26985	A26838	VHWV	A35694	T41455	A23101	W5WL39	A61594	D71541	T02683	A47196
7	7	7	~	7	7	7	-1	~	N	7	Н	N	0	~	7
771	926	926	926	957	1021	1046	1253	1827	1828	58	72	84	115	174	185
63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	63.5	61.5	61.5	61.5	61.5	61.5	61.5
33	33	33	33	33	33	33	33	33	33	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1 T25817 hypothetical protein K12D9.3 - Caenorhabditis elegans C;Species: Gaenorhabditis elegans C;Species: Gaenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T25817 R;Graves, T R;Graves, T R;Graves, T R;Graves, T R;Graves, T R;Graves, T R;Graves, C	orhabditis elegans ion 15-Oct-1999 #text_change 15-Oct-1999 November 1996 legans cosmid K12D9.
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-297 <gra> A;Cross-references: EMBL:U80030; PIDN:AAB37600.1; GSPDB:GN00023; CESP:K12D9.3 A;Experimental source: strain Bristol N2; clone K12D9 C;Genetics: A;Gene: CESP:K12D9.3 A;Map position: 5 A;Introns: 165/3; 208/3</gra>	rom GB/EMBL/DDBJ DN:AAB37600.1; GSPDB:GN00023; CESP:K12D9.3 ol N2; clone K12D9
Query Match	Score 39; DB 2; Length 297; Pred. No. 14; ; Mismatches 1; Indels 0; Gaps 0;

Cispecies: Neisseria meningitidis
Cispecies: Neisseria: Nei

A;Gene: argC; NMA0676 C;Superfamily: N-acetyl-gamma-glutamyl-phosphate reductase C;Keywords: oxidoreductase

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Gaps

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phage-related endolysin XF0513 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Accession: D82795
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A2515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-154 <SINA
A; Cross-references: GB:AE003900; GB:AE003849; NID:g9105366; PIDN:AAF83323.1; GSPDB:GN001
A; Experimental source: strain 9a5c
R; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinard, P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Alvarenga, R.; F Briones, M.R.S.; Buenco, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Alvarenga, R.; F as-Neto, E.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
as-Neto, E.; Docena, C.; Bl-Dorry, H.; Fraciani, A.P.; Franca, S.C.; Franco, M.C.; Frobm S; Matthors: Ferreira, V.C.A.; Ferreira, J.D.; Vittajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrado, M.A.; Madeira, A.M. B.N.; Madeira, H.M.F.; Martins, E.M.F.; Matthors: Martins, E.M.F.; Matthors: Martins, E.M.F.; Matthors: C.F. Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawash A; Atthors: as Silva, A.J.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvei, N.A.; Verjovski-Almeida, S.; Vettore, A.L.; E.J.; A.R.Eference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T30B22.1 - Arabidopsis thaliana (5.8pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: 0.1Feb-1999 #sequence_revision 0.1Feb-1999 #text_change 24-Nov-1999 (5.5acession: T00416 (5.5acession: T00416 (5.5acession: T00416 (5.5acession: T00416 (5.5acession: A.) Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc Bubmitted to the BMBL Data Library, October 1998 (5.5acesription: Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence. A;Reference number: 214149
              J. Invest. Dermatol. 91, 541-546, 1988
A.Title: Cloning and characterization of a mouse type I hair keratin cDNA.
A.Reference number: A46559; MUID:89054860; PMID:2461417
A.Accession: A46559
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-416 -6BEA
A.Residues: 1-416 -6BEA
A.Coss-references: GB:M27734; NID:g198585; PIDN:AAA39372.1; PID:g198586
C; Superfamily: cytoskeletal keratin
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Pred. No. 11;
2; Mismatches 0; Indels
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: D82795
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R/Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A,Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Reference number: A81000; MUID:2017575; PMID:10710307

A;Reference number: A81000; MUID:2017575; PMID:10710307

A;Retsis: preliminary

A;Residues: 1-347 <TET>
                                                                                                                                                                                                                                                                                                                                                                              N-acetyl-gamma-glutamyl-phosphate reductase NMB1787 [imported] - Neisseria meningitidis C;Species: Neisseria meningitidis C;bate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE002528; GB:AE002098; NID:g7227034; PIDN:AAF42126.1; PID:g722704
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kaytes, P.S.; McNab, A.R.; Rea, T.J.; Groppi, V.; Kawabe, T.T.; Buhl, A.B.; Bertolino, J. Invest. Dermatol. 97, 815-842, 1991
A;Title: Hair-specific Keratins: characterization and expression of a mouse type I kerat
A;Reference number: A61404; MUID:92013235; PMID:177610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        keratin, type I, hair (clone MHKA-1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 13-Aug-1999
C;Accession: A46559
R;Bertolino, A.P.; Checkla, D.M.; Notterman, R.; Sklaver, 1.; Schiff, T.A.; Freedberg,
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.Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 03-May-1996
                                                                                    Gaps
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A;Staus: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: CAX>
C;Superfamily: cytoskeletal keratin
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              Length 347;
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          Score 39; DB 2
Pred. No. 16;
2; Mismatches
          75.0%;
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Best Local Similarity 75.0%;
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156 CVSLPLVP 163
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| CVSLPLVP 163
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Gaps

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A;Cross-references: GB:AE000637; GB:AE000511; NID:g2314536; PIDN:AAD08412.1; PID:g231453 C;Genetics:
A;Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: H64690
R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKennel son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A64520; MUID: 97394467; PMID: 9252185
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A;Molecule type: DNA
A;Residues: 1-407 <WIL.)
A;Coss-references: EMBL:281048; PIDN:CAB02841.1; GSPDB:GN00019; CESP:C41G7.4
A;Experimental source: clone C41G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA A,Residues: 1-287 <TOM>
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19895
R;Steward, C.
submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                             type IIS restriction enzyme M2 protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                      C,Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 22-Jun-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                       0;
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                           Length 3623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 2; Length 287; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C41G7.4 - Caenorhabditis elegans
                                 DB 2; I
2.3e+02;
                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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                                 Score 38;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.2%; Score 37; 66.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 1
A;Introns: 27/2; 107/3; 151/3; 333/3; 373/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.2%;
75.0%;
                                 73.18;
66.78;
                              Query Match 73.1
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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                                                                                                                                                                                    313 CSQAPLVPC 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: Z19192
A;Accession: T19895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|||:|
86 CINVPLMP 93
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                1 CISVPLVPC
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A;Gene: CESP:C41G7.4
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Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accession: T08618
R;Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998
A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies A;Reference number: Z16459; MUID:98148073; PMID:9478979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-3523/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F;133-164/Domain: EGF homology <EGF>
F;436-467/Domain: EGF homology <EGF>
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;Molecule type: mRMs
FResidues: 1-3623 <MOE>
;Cross-references: EMBL:AF022247; NID:g3834379; PIDN:AAC71661.1; PID:g3834380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: Dna. A;Residues: 1-1015 <STO> A;Cross-references: GB:AE002093; NID:g3738282; PIDN:AAC63624.1; GSPDB:GN00139 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable ATP-dependent RNA helicase A [imported] - Arabidopsis thaliana C,Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: C84918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intrinsic factor-B12 receptor CUBILIN precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                 A, Residues: 1-577 <ROUS
A, Residues: 1-577 <ROUS
A, Cross-references: EMBL:AC002535; NID:g2529657; PID:g2529658
A, Experimental source: cultivar Columbia
C; Genetics: A, A, Map position: A, A, A, A, A, B, 11 L Cons. 87/3; 126/3; 175/1; 264/3; 329/3; 507/3
C; Superfamily: Arabidopsis thaliana hypothetical protein T30B22.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.1%; Score 38; DB 2; Length 1015; 75.0%; Pred. No. 68; 1; Indels :ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                  Score 38; DB 2; Length
Pred. No. 40;
1; Mismatches 1; Inde
A;Accession: T00416
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                     73.1%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.1
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 CVSVPFVP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVSVPFVP 683
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Best Local Similarity
Matches 6; Conserv
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                                                         A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: At2g47680
A;Map position: 2
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à g 0;

Gaps

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Length 278 1; Indels

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A;Cross-references: GB:AL513382; PIDN:CAD09512.1; PID:g16504629; GSPDB:GN00176 C;Genterics: AT93756 C;Superfamily: hypothetical protein b2382
                                                                                                                                                                       Score 35; DB 2;
Pred. No. 68;
2; Mismatches
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                                                                                                                                                                       Query Match 67.3
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
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Job time: 7.90909 secs
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56 ITAPLIPC 63
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Best Local Similarity
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SIPIIPC 9
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A;Molecule type: DNA
A;Residues: 1-305 <SIM>
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        A;Residues: 1-278 <PAR>
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G;Species: Salmonella enterica subsp. enterica serovar Typhi
G;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
G;Accession: AF0936
R;Parkhill, J: Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Althors: Parry, C.; Quail, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Althors: Omplete genome sequence of a multiple drug resistant Salmonella enterica serov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.; Biss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Accession: JQ1086 S. S. Van der Knaap, E.; van de Wiel, C.; van Kammen, A.; Bis R,Scheres, B.; van Eggelen, F.; van der Knaap, E.; van de Wiel, C.; van Kammen, A.; Bis Plant Cell 2, 687-700, 1990 A.; Plant Cell 2, 687-700, 1990 A.; Van Gene expression in the developing pea nodule. A;Reference number: JQ1084; MUID:93005665; PMID:2152123
                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1639 <SEE.
A;Cross-references: EMBL:AL157734; PIDN:CAB75776.1; GSPDB:GN00066; SPDB:SPAC1834.08
A;Experimental source: strain 972h(-); cosmid c1834
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C;Species: Pisum Bativum (garden pea)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 20-Apr-2001
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
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A;Residues: 1-61 <SCH>
A;Cross-references: GB:S45162; NID:g257036; PIDN:AAB23538.1; PID:g257037
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                                                                         R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, February 2000
A;Reference number: Z25039
A;Accession: T50119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 2; Length 163
Pred. No. 2.5e+02;
1; Mismatches 0; Indels
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F;1-20/Domain: signal sequence #status predicted <SIG>F;21-61/Product: nodulin 14 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: root nodule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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NIPLVPC 27
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A;Molecule type: DNA
                                                          Accession: T50119
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A; Introns: 23/3
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Conserved hypothetical protein XF1068 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: A82728
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:0910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; restructed: 1-30 - S.17.
A; restructes: GB:AE003943; GB:AE003849; NID:g9106006; PIDN:AAF83878.1; GSPDB:GN001
A; Experimental source: strain 9aSc
B; Sidmpson, A.JG:Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; P
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.R.; Camargo, L.E.A.; Carraro, D.M.; Carrer, A
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
A; Authors: Perreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Unqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laign-
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Marsukuma, A.Y.; Marino, C.L.; Marques, W.V.; Martins, E.M.F.; Marsukuma, A.Y.; Menork, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.Y.
A; Muthors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvain, M.Y.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski.Almeida, S.; Vettore, A.L.; A.L.; Z.
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Pred. No. 74;
3; Mismatches 0; Indels
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 5, 2004, 09:38:39 ; Search time 4.09091 Seconds
(without alignments)
114.554 Million cell updates/sec Run on:

US-09-761-636A-14 52 1 CISVPLVPC 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	m einessien Stwie	eria Pria	61765 mus muscul			cucum	5 oryctola			_			mus m	Q98sp7 brachydanio				Q10866 mycobacteri	Q8xd64 escherichia			_	P03315 semliki for	P18296 schizosacch		-			_	_			7190 escher
SUMMARIES		ARGC NEIMA	ARGC_NEIMB	K1M1 MOUSE	NO14 PEA	VES HPV70			11	OCN3_HUMAN		SYEP_HUMAN	RN27_HUMAN	RN27_MOUSE	BBS2_BRARE	M172_HUMAN	TSP1_XENLA	NU4M_ACACA	CTPG_MYCTU	XDHD_ECO57	XDHD_ECOLI	DPOM_NEUCR	PSTA_DICDI	POLS_SFV	CUT1_SCHPO	VE5_HPV39	٠,						NRT1_CHICK	GATD_ECOLI
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	Result No.	1	7	ю	4	S	9	7	ω (		01:	17.	77	13	14	12	16	17	18	19	50	21	22	570	4.1	52	970	2.7	58	53	30	31	32	33

P37059 homo sapien	P43429 rattus norv	Q01657 chlamydomon	076013 homo sapien	09kv59 vibrio chol	P58021 mus musculu	099805 homo sapien	Oguhié homo sanien	028178 bos taurus	P07996 homo ganien	P35441 mus musculu
DHB2_HUMAN	GAT1_RAT	RSP6_CHLRE	KIM6 HUMAN	ACSA_VIBCH	T9S2 MOUSE	T9S2 HUMAN	DD20 HUMAN	TSP1_BOVIN	TSP1_HUMAN	TSP1_MOUSE
~ ~	• ~	Н	Н	Н	-+	Н	Н	Н	Н	7
387	413	459	467	649	662	663	824	1170	1170	1170
61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5
322	32	32	32	32	32	32	32	32	32	32
3.34 5.75	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

DB 1; Length 347; 75.0%; Score 39;

Query Match

Pred. No.

75.0%;

Best Local Similarity

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-QUT-2001 (Rel. 40, Last annotation update)
Keratin, type I cuticular HAI (Hair Keratin, type I HAI) (HKA-1)
KRTHAI OR KRTI-1 OR HKAI.
                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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364
92
103
204
220
305
416 AA;
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Best Local Similarity
Matches 6; Conserv
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NO14 PEA
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MEDLINE-2017575; PubMed=10710307;
MEDLINE-2017575; PubMed=10710307;
Eisen J.A., Katchum K.A., Heidelberg J., Jeffries A.C., Nelson K.E.,
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey B.K.,
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark B.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Golton M.D., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+) + phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
-i- PATHWAY: Arginine biosynthesis; third step.
-i- SUBCELLULA. LCCATION: Cytoplasmic (Probable).
-i- SUBCELLULA. Belongs to the NAGSA dehydrogenase family. Subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  28-FZB-2003 (Rel. 41, Last sequence update)
10-607-2003 (Rel. 42, Last annotation update)
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; NWB.100/1.

HAMAP; NWB.10050. -; 1.

HAMAP; WF 00150. -; 1.

InterPro; IPR000706; AGPR act site.

InterPro; IPR000534; Semialdh_dh.

Pfam; PF021118; Semialdhyde_dh; 1.

Pfam; PF02174; Semialdhyde_dh; 1.

Procon; P003755; AGPR act site; 1.

PROSITE; PS01224; ARGC; FALSE NEG.

Arginine biosynthesis; Oxidoreductase; NADP; Complete proteome.

152

BILLARITY.

152

BILLARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
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Pred. No. 4.2;
2; Mismatches (
ed. No. 4.2;
Mismatches
                                                                                                                                                                                                                                                                                                                          347 AA
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                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 41, Created)
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75.0%;
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                                 6; Conservative
                                                                                                                                                                                                                                                                                                                              STANDARD;
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156 CVSLPLVP 163
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Beet Local Similarity
6, Conserve
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156 CVSLPLVP 163

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                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                        J. Invest. Dermatol. 91:541-546(1988).

-!- MISCELLANEOUS: THERE ARE TWO TYPES OF HAIR/MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUB=Hair;
MEDLINE=89054860; PubMed=2461417;
Bertolino A.P., Checkla D.M., Notterman R., Sklaver I., Schiff T.A.,
Freedberg I.M., Didona G.J.,
"Cloning and characterization of a mouse type I hair keratin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;

    -!- SIMILARITY: Belongs to the intermediate filament family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO14_PEA STANDARD; PRT; 61 AA. P26415; 01-AUG-1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coil; Keratin.
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COIL 2.
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COIL 1A.
LINKER 1.
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InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
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ENOD14.
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CVSVPQVLC 93
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Best Local Similarity
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                                                     Early protein
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Matches
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Matches
                                                                                                                                                                                                             RESULT 6
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SO WE BER
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                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                             -!- MISCELLANEOUS: CONTAINS 4 CYSTEINES ARRANGED IN TWO PAIRS IN SUCH
A WAY THAT THEY MIGHT BE CAPABLE OF BINDING A METAL ION.
-!- SIMILARITY: TO NODULIN 3.
                                                                                                                                                                                    -!- DEVELOPMENTAL STAGE: Expressed in the second stage of root nodule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
           Eukaryota, Viridiplantãe, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
                                                                                     STRAIN=CV. Sparkle; TISSUB=Root nodules; MEDLINE=93005665; PubMed=2152123; MEDLINE=93005665; PubMed=2152123; MEDLINE=93005665; PubMed=2152123; MEDLINE=93005665; PubMed=2152123; Van der Knaap E., van de Wiel C., van Kammen A., Bisseling T.; "Sequential induction of nodulin gene expression in the developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=96249586; PubMed=8815087;
Forslund O., Hansson B.G.;
Human papillomavirus type 70 genome cloned from overlapping PCR
products: complete nucleotide sequence and genomic organization.";
J. Clin. Microbiol. 34:802-809(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 1; Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type 70.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=39457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         D508059695F62B8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Probable ES protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           NODULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                          EMBL; S45162; AAB23538.1; -.
PIR; JQ1086; JQ1086.
Nodulation; Signal; Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        7175 MW;
                                                                                                                                                         nodule.";
nt Cell 2:687-700(1990)
Pisum sativum (Garden pea)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|||||
21 NIPLVPC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SVPLVPC 9
                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AA;
                                                   NCBI_TaxID=3888;
                                                                                                                                                                                                   formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VES HPV70
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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SIGNAL
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                                                                                                                                                                         Plant
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                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the cucumoviruses/bromoviruses 3A family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim S.H., Park Y.I.;
Submitted (JuL-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIALLY
INFECTED CELLS TO ADJACENT CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cucumber mosaic virus (strain As) (CMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Lagomorpha, Leporidae; Oryctolagus.
NCBI_TaxID-9986;
                                                                                                                                                                                                                                                             ;
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15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last amouation update)
Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%; Score 35; DB 1; Length 279;
66.7%; Pred. No. 19;
.ive 1; Mismatches 2; Indels
                                                                                                                                                                                           Score 35; DB 1; Length 78;
Pred. No. 5.2;
                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30509 MW; 2B47059288DC1069 CRC64;
                                                                                                                              DFEA59CB355042D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell-to-cell movement protein (MP) (3A protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 AA.
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                                                                                                                                                                                                                                                          1; Mismatches
EMBL, U21941; AAC54855.1; -.
InterPro; IPR004270; Papilloma_E5.
Pfam; PF03025; Papilloma_E5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF013291; AAB67166.1; -.
                                                                                                                                                                                           67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR000603; 3A_mov. Pfam, PF00803; 3A, 1. DNA-binding; Transport.
                                                                                                                                  78 AA; 9262 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                          6; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                   BGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROXYLATION (BY SIMILARITY).
CHARGE RELAY SYSTEM.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
20ganic cation transporter 3 (Solute carrier family 22, member 3).
SLC22A3 OR OCT3.
Rattus norvegicus (Rat).
      ACTIVATED FACTOR XA, HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                         (BY
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                                                                       GAMMA-CARBOXYGLUTAMIC ACID (BY
                                                                                                                                         (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                 GAMMA-CARBOXYGLUTAMIC ACID SIMILARITY).
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GAMMA-CARBOXYGLUTAMIC ACID
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                                                                                                                        SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
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                                                         SERINE PROTEASE
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0; Mismatches
                                                                                                                                                                                                                                                                                          SIMILARITY).
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     490
122
165
490
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490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta;
      233
86
125
233
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088446;
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CARBOHYD
SEQUENCE
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DISULFID
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MOD_RES
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                      DOMAIN
DOMAIN
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MEDLINE-9726311; PubMed=9101642;

MEDLINE-9764119; Pareferential clawage: Acg. | Thr and then converts prothrombin to thrombin of conting.

MARY-1-11e bonds in prothrombin to form thrombin.

MARY-1-11e bonds in gresidues and are held together by 1 or more disulfide bonds.

MOTHER THE VITAMIN K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium (By
                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation; Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K; Signal; Zymogen; EGF-like domain; Repeat.
                                                                                                                                                                                                                                                                              PTM: N- and O-glycosylated (By similarity).

PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                       -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to another alte, beyond the GLA domain.
-1- SIMILARITY: Belongs to peptidase family 51.
-1- SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIĂL.
BY SIMILARITY.
FACTOR X LIGHT CHAIN.
FACTOR X HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SW00020; Tryp, SPC; 1.
PROSITE; P800010; ASX HYDROXYL; 1.
PROSITE; P8000102; EGF 2; 2.
PROSITE; P850026; EGF 3; 1.
PROSITE; P850026; EGF 3; 1.
PROSITE; P801187; EGF 2; 1.
PROSITE; P801187; EGF 2, 1.
PROSITE; P850240; TRYPEIN DOM; 1.
PROSITE; P850240; TRYPEIN DOM; 1.
PROSITE; P850240; TRYPEIN DIM; 1.
PROSITE; P800134; TRYPEIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; DY12.10, 1.
InterPro; IPR00015; Asx hydroxyl S.
InterPro; IPR00003; Cyg_Ser_trypsin.
InterPro; IPR00183; EGF_2.
InterPro; IPR00183; EGF_II.
InterPro; IPR00183; EGF_II.
InterPro; IPR001293; GLA_DIOAC.
InterPro; IPR001293; GLA_DIOAC.
InterPro; IPR001294; Peptidase_SIA.
InterPro; IPR001314; Peptidase_SIA.
InterPro; IPR001314; Peptidase_SIA.
InterPro; IPR001314; Peptidase_SIA.
InterPro; IPR001314; Peptidase_SIA.
InterPro; IPR001294; Peptidase_SIA.
InterPro; IPR001294; Glay.
Pfam; Pr00089; EGF; 2.
Pfam; Pr00089; LTYPBAIN; 1.
PRINTS; PR00010; GTRMCTRYPSIN.
PRINTS; PR00010; GTRMCTRYPSIN.
PRINTS; PR00010; GTRMCTRYPSIN.
SMART; SM00179; EGF_CA; 1.
SMART; SM00179; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF003200; AAB62542.1; -. HSSP; P00742; 1HCG.
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490
232
                                                                                                                                                                                                                                                                          similarity)
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CHAIN
PROPEP
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o,

Gaps

6

556 AA

STANDARD;

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MIM;
                                                                                                                                                                                                                    TISSUE-Placenta;

M. 125. TISSUE-Placenta;

M. X., Kekuda R., Huang W., Fei Y.-J., Leibach F.H., Chen J.,

A. Conway S.J., Ganapathy V.;

A. Conway S.J., Ganapathy V.;

A. Conway S.J., Ganapathy V.;

A. Tidentity of the organic cation transporter OCT3 as the extraneuronal monoamine transporter (uptake2) and evidence for the expression of the transporter in the brain...

T. Biol., Chem. 273:32776-32786(1998).

J. Biol., Chem. 273:32776-32786(1998).

- FUNCTION: Mediates potential-dependent transport of a variety of organic cations. May play a significant role in the disposition of cationic neurotoxins and neurotransmitters in the brain.

- SUMCELIOUAR LOCATION: Integral membrane protein.

- ISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA WITH MODERATE EXPRESSED, ESPECIALLY IN HIPPOCAMPUS, CEREBELLUM AND CEREBRAL

- COPTEX: EXPRESSION IS LOW IN KIDNEY AND UNDETECTABLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                "Cloning and functional characterization of a potential-sensitive, polyspecific organic cation transporter (OCT3) most abundantly expressed in placenta.";
        Kekuda R., Prasad P.D., Wu X., Wang H., Fei Y.-J., Leibach F.H., Ganapathy V:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the sugar transporter family. Organic cation subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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InterPro; IPRO04749; Orgoat transp.
InterPro; IPRO05829; Sub_transporter.
InterPro; IPRO05829; Sug_transporter.
Pfam; PF00083; sugar_tr; 1.
ITGRFAMs; TICR00896; ZA0119; 1.
PROSITE; PSS00216; SUGAR_TRANSPORT 1; 1.
PROSITE; PSS00216; SUGAR_TRANSPORT 1; 1.
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                                                                                                                                                                    Biol. Chem. 273:15971-15979(1998)
  MEDLINE=98298098; PubMed=9632645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99134299; PubMed=9933568;
Verhaagh S., Schweifer N., Barlow D.P., Zwart R.;
"Cloning of the mouse and human solute carrier 22a3 (Slc22a3/SLC22A3)
identifies a conserved cluster of three organic cation transporters on
mouse chromosome 17 and human 6q26-q27.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lerangporter OCT3 in the kidney.";
Am. J Physiol. 279.F449-F458(2000).
-!- FUNCTION: Mediates potential-dependent transport of a variety of organic cations. May play a significant role in the disposition of cationic neurotoxins and neurotransmitters in the brain.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUB SPECTRICITY: EXPRESSED IN PLACENTA, SKELETAL MUSCLE, PROSTATE, AONTA, LIVER, FETAL LUNG, SALIVARY GLAND, ADRENAL KIDNEY AND BRAIN CORTEX. NO EXPRESSION DETECTED IN SPLEEN.
-!- SIMILARITY: Belongs to the sugar transporter family. Organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20425388; PubMed=10966924; Wu X., Huang W., Ganapathy M.E., Wang H., Kekuda R., Conway S.J., Lelbach F.H., Ganapathy V.; "Structure, function, and regional distribution of the organic cation transporter OCT3 in the kidney.";
              075751; Q9UP02;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Organic cation transporter 3 (Extraneuronal monoamine transporter)
(EMT) (Solute carrier family 22, member 3).
                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0015101; F:organic cation transporter activity; TAS.
GO; GO:0015695; P:organic cation transport; TAS.
                                                                                                                                                                                                                                                                                                                           Gruendemann D., Schechinger B., Rappold G.A., Schoemig E., "Molecular identification of the corticosterone-sensitive extraneuronal catecholamine transporter.";
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 513-556 FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transport; Ion transport; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY
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PS00217; SUGAR TRANSPORT 2; FALSE NEG.
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InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
                                                                                                                                                                                                                                                                                                          MEDLINE=99212254; PubMed=10196521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                           Nat. Neurosci. 1:349-351(1998).
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TIGRFAMs; TIGR00898; 2A0119; 1.
PROSITE; PS50850; MFS; 1.
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                                                                                                                                                                    Homo sapiens (Human)
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TISSUE=Kidney;
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Gaps

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1; Indels

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RESULT 9 OCN3\_HUMAN

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EMBL; X54326; CAA38224.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                        transferase involved in cell wall arabinan biosynthesis that is the target for the antimycobacterial drug ethambutol.";
Proc. Natl. Acad. Sci. U.S.A. 93:11919-11924(1996).
-!- FUNCTION: Arabinosyl transferase responsible for the polymerization of arabinose into the arabina of arabinosal arabinose into the arabina of arabinosal sci. SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: BELONGS TO THE EMB FAMILY.
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                              POTENTIAL.
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N.LINKED (GLCNAC. . . ) (POTENTIAL).
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Belanger A.E., Besra G.S., Ford M.E., Mikusova K., Belisle J.T.,
Brennan P.J., Inamine J.M.;
                                                                                                     (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                        Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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Pfam; PF04602; arab transf; 1.
Transferase; Glycosyltransferase; Transmembrane; Cell wall;
                                                                                                                              Score 35; DB 1; Length 556; Pred. No. 40;
                                                                                                                                                      1; Indels
                                                                                                               C3CA2D77DD21C658 CRC64;
                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable arabinosyltransferase A (EC 2.4.2.-)
                                                                                                      N-LINKED (GLCNAC
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                                                                                                                556 AA;
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                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1764;
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P71485;
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MEDLINE=88262551; PubMed=3290852;

MEDLINE=88262551; PubMed=3290852;

Thoemnes P., Fett R., Schray B., Kunze N., Knippers R.;

The core region of human glutaminyl-tRNA synthetase homologies with

RT the Escherichia coli and yeast enzymes.";

RL Nucleic Acids Res. 16:391-5406 (1988).

C. -i- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +

diphosphate + L-glutamyl-tRNA(Glu).

C. CATALYTIC ACTIVITY: ATP + L-proline + tRNA(Pro) = AMP +

diphosphate + L-prolyl-tRNA(Pro).

C. CATALYTIC Component of the multisynthetase complex which is

c. Gomprised of a bifunctional glutamyl-prolyl-tRNA synthetase,

C. SUBLINAT: component of the multisynthetase as well as three auxiliary

proceins, pl8, p48 and p43.

C. SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CLASS-II

AMINOACYL-TRNA SYNTHETASE FAMILY.

C. SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CLASS-II

AMINOACYL-TRNA SYNTHETASE FAMILY.

C. SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CLASS-II

AMINOACYL-TRNA SYNTHETASE FAMILY.

C. SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CLASS-II

AMINOACYL-TRNA SYNTHETASE FAMILY.

C. SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CLASS-II

AMINOACYL-TRNA SYNTHETASE FAMILY.

C. SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CLASS-II

AMINOACYL-TRNA SYNTHETASE FAMILY.

C. STANILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CLASS-II

AMINOACYL-TRNA SYNTHETASE FAMILY.

C. STANILARITY: IN THE C-TERMINAL SECTION, BELONGS TO CLASS-II

AMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The primary structure of human glutaminyl-tRNA synthetase. A highly conserved core, amino acid repeat regions, and homologies with translation elongation factors."; J. Biol. Chem. 266:1448-1455(1991).
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAT-1998 (Rel. 08, Created)
01-MAT-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bifunctional aminoacyl-tRNA synthetase [Includes: Glutamyl-tRNA synthetase (EC 6.1.1.77) (Glutamate--tRNA ligase); Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase);
EPRS OR QRS OR GLNS OR PARS.
HOMO sapiens (Human)
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-!- CAUTION: Was originally thought to be a glutaminyl-tRNA
                                                                                                                                                                                                 Score 35; DB 1; Length 1108;
                                                                                                                                                                                                                                                                                            0; Indels
                                                                         696 718 POTENTIAL.
1108 AA; 117404 MW; 0ED8E648768075FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1440 AA.
                                                                                                                                                                                                                                                 Pred. No. 81;
3; Mismatches
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                                               POTENTIAL.
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MEDLINE=91107633; PubMed=1988429;
Fett R., Knippers R.;
                                                                                                                                                                                                                   67.3%;
                                                                                                                                                                                                                                                     62.5%;
                                                                                                                                                                       Query Match
Best Local Similarity 62.35,
1748 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
638
675
718
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28 CLAVPLLP 35
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CONFLICT
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                                                                              DR WINK: 1910; DEKEN.

BR GO; GO:00005625; C:soluble fraction; TAS.

GO; GO:0005625; C:soluble fraction; TAS.

BR GO; GO:0006525; C:soluble fraction; TAS.

BR GO; GO:0006461; P:protein complex assembly; TAS.

BR InterPro; IPR004924; Gluz ERNA-synt_IC.

BR InterPro; IPR004046; GST_Cterm.

BR InterPro; IPR00412; FRNA-synt_IC.

BR InterPro; IPR001412; FRNA-synt_IC.

BR InterPro; IPR001412; ERNA-synt_IC.

BR Pfam; PF00142; ERNA-synt_IC.

BR Pfam; PF00143; ERNA-synt_IC.

BR Pfam; PF00143; ERNA-synt_IC.

BR Pfam; PF00144; IRNA-synt_IC.

BR Pfam; PF00145; IRNA-synt_IC.

BR Pfam; PF00146; IRNA-Synt_IC.

BR PROSITE; PS00176; AA TRNA-IGGSE I;

BR PROSITE; PS00176; AA TRNA-IGGSE I;

BR PROSITE; PS00172; AA TRNA-I
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
(Tripartite motif-containing protein 8).
TRIMS OR RNF27 OR GERP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PROLYI-TRNA SYNTHETASE.
"HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163026 MW; C4E185A0AA41C204 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multifunctional enzyme; Repeat; 3D-structure.
DOMAIN 92 687 GLUTAMYL-TRNA SYNTHETASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 1; I
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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WHEP-TRS 2.
WHEP-TRS 3.
CHARGED.
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MEDLINE=20568703; PubMed=11118312;
Vincent S.R., Kwasnicka D.A., Fretier P.;
    EMBL; X07466; CAA30354.1; ALT SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 44.4
es 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                   PIR, A38663; SYHUQT.
PDB; 1FYJ; 31-DEC-02.
Genew, HGNC:3418; EPRS.
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132
360
363
688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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11D DT
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RT 34 novel RING finger= Box-colled coll procenn GRRP.";

Biochem Biophys Res. Commun. 279:482-486(2000).

RN [1]

RN [1]

RN [2]

RN
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RESULT 14
BBS2_BRARE
ID BBS2_BRARE
                                                                                                                                                                                                                            28-FEB-2003
28-FEB-2003
                               DOMAIN
CONFLICT
SEQUENCE
                                                                              Query Match
Best Local S
ZN_FING
ZN_FING
DOMAIN
                                                                                                                                                                                                                  Q98SP7;
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M172_HUMAN
                                                                                                    Matches
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  STATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBUNIT: Homodinier (By similarity).
-1- SUBCELLUIAR LOCATION: Nuclear (By similarity).
-1- SUBCELLUIAR LOCATION: Nuclear (By similarity).
-1- DEVELOMENTAL STAGE: At 10.5 and 12.5 dpc, expressed in the central nervous system. At 14.5 dpc, expressed in the eye (lens and inner neural layer of the retina), in the primitive glomeruli of the developing kidney, in the villi of the gut and in the dorsal root ganglia.
-1- DOMAIN: The coiled coil domain is required for homodimerization (By similarity).
                        Gaps
                                                                                                                                     099572; 099pQ4;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
RING finger protein 27 (Glioblastoma-expressed ring finger protein)
(Tripartite motif protein 8).
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21231161; PubMed=11331580; Reymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Luzi L., Reymond A., Meroni G., Fantozzi A., Merla G., Cainarca S., Guffanti A., Minucci S., Pelicci P.G., Ballabio A.; "The tripartite motif family identifies cell compartments."; EMBO J. 20:2140-2151(2001).
                        ö
   DB 1; Length 551;
                       1; Indels
                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=20568703; PubMed=11118312;
Vincent S.R., Kwasnicka D.A., Fretier P.;
"A novel RING finger-B box-coiled-coil protein, GERP.";
Biochem. Biophys. Res. Commun. 279:482-486(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 RING-type zinc finger.
                                                                                                                             551 AA
             Pred. No. 61;
0; Mismatches
    Score 34;
                                                                                                                            PRT;
    65.4%;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 196-463 FROM N.A.
                           6; Conservative
                                                                                                                             STANDARD;
                                                                    361 ŚVPĽYPC 367
                                                                                                                                                                                                                      Mus musculus (Mouse)
                                               3 SVPLVPC 9
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                              RN27 MOUSE
                           Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxIb=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M172 HUMAN STANDARD; PRT; 966 AA.
Q14596; Q13173; Q15026; Q96GB6; Q9NRF7;
Q14597 (Rel. 35, Created)
Q18-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Membrane component, chromosome 17, surface marker 2 (Next to BRCA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21181710; PubMed=11285252; MEDLINE-21181710; PubMed=11285252; MIShimura D.Y., Sarby C.C., Carmi R., Elbedour K., Van Maldergem I Fulton A.B., Lam B.L., Powell B.R., Swiderski R.E., Bugge K.E., Haider N.B., Kwitek-Black A.E., Ying L., Duhl D.M., Gorman S.M., Heon E., Iannaccone A., Bonneau D., Biesecker L.G., Jacobson S.G., Stone E.M., Sheffield V.C., a novel gene on chromosome 16q causing "Positional cloning of a novel gene on chromosome 16q causing Bardet-Biedl syndrome (BBS2)."; Hum. Mol. Genet. 10:865-874 (2001).
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                                                                                                                                                                            65.4%; Score 34; DB 1; Length 551; 85.7%; Pred. No. 61;
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                                                                                                      G -> A (IN REF. 2).
CECB2D70C8B1E0B6 CRC64;
                                                   COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         715 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                  0; Mismatches
B BOX-TYPE 1.
B BOX-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Last annotation up
Bardet-Biedl syndrome 2 protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZFIN, ZDB-GENE-020801-1; bbs2.
InterPro; IPRO00413; Integrin_alpha.
Pfam; PF01839; FG-GAP; 2.
SEQUENCE 715 AA; 79125 MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF342739; AAK28555.1; -.
                                                                                                                                 61591 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
     132
182
249
295
259
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                                                                                                                                                                                                                                                                                                                                           361 SVPLYPC 367
     92
140
181
274
259
551 AA;
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                        3 SVPLVPC 9
                                                                                                                                                                                                         Similarity
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TISSUE=Testis;
                                 BRCAl gene.";
                                 Hum. Mol
```

IsoId=Q14596-1; Sequence=Displayed;

```
ISOId=Q14596-2; Sequence=VSP 004314;
Note=No experimental confirmation available;
-!- SIMILARITY: Contains 1 UDR domain.
-!- SIMILARITY: Contains 1 ZZ-type zinc finger.
-!- SIMILARITY: Contains 1 ZZ-type zinc finger.
-!- CAUTION: Was originally (Ref.1) thought to be the ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Job time : 5.09091 secs
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DOMAIN
VARSPLIC
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Matches
          MEDINE-2238257; PubMed-12477932;

WEDINE-2238257; PubMed-12477932;

Attacher R.D., Collins F.S., Wagner L.H., Derge J.G.,

Attschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Doardseln M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muruy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Colling A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

"Thuman and mouse Colk."
                                                                                                                                                                                           TISSUE=Ovary;
MEDLINE=94348506; PubMed=8069304;
Campbell I.G., Nicolai H.M., Foulkes W.D., Senger G., Stamp G.W.,
Allan G., Boyer C., Jones K., Bast R.C. Jr., Solomon E., Trowsdale J.,
Black D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dimitrov S., Brennerova M., Forejt J., "Expression profiles and intergenic structure of head-to-head oriented Brcal and Nbrl genes."; Gene 262:89-98 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96051398; pubMed=7584044;
Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.;
"Prediction of the coding sequences of unidentified human genes. II.
The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by
analysis of CDNA clones from human cell line KG-I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [5]
SEQUENCE OF 412-508 FROM N.A.
MEDLINE=96090243; PubMed=7581362;
Harshman K., Bell R., Rosenthal J., Katcher H., Miki Y.,
Swenson J., Gholami Z., Frye C., Ding W., Dayananth P.,
Swenson K., Norris F.H., Bristow P.K., Phelps R., Hattier T.,
Stone S., Shaffer D., Bayer S., Hussey C., Tran T., Lai M.,
Rosteck P.R., Skolnick M.H., Shattuck-Eidens D., Kamb A.;
"Comparison of the positional cloning methods used to isolate the
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                        "A novel gene encoding a B-box protein within the BRCAl region at
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT HIS-923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
gene 1 protein) (1A1-3B).
M17S2 OR NBR1 OR 1A13B OR KIAA0049.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Genet. 4:1259-1266(1995).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21100444; PubMed=11179671;
                                                                                                                                                                                                                                                                                                                                                                            Hum. Mol. Genet. 3:589-594(1994).
                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-42 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Bone marrow;
                                                                                                                       NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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PIISEDQTAALMARLFEMGFCDRQLNLRLLKKHNYNILQVV
PIELLQLNNNNDWYSQRY -> GLWGLLSFLHLAKKCFFLKAP
SEAFGWF (in iseform 2).
/FIId=VSP_004314.
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Pred. No. 1.18+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FILE -> H (in dosn): 1054385).
/FILE-VAR 016106.
LGDSMYSSALSQPGLERGAEGKPGV -> QAWSEVLKASLGF (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          966 AA; 107432 MW; 6A057E7AA88BEAEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000270; OPR PB1.
InterPro; IPR000449; UBA_domain.
InterPro; IPR000449; UBA_domain.
InterPro; IPR00043; Znf_ZZ.
Pfam; PF00564; PB1; 1.
Pfam; PF00569; ZZ! 1.
SMART; SM000591; ZnF_ZZ; 1.
SWART; SM000591; ZnF_ZZ; 1.
PR0SITE; PS50030; UBA; 1.
PROSITE; PS501357; ZF_ZZ_1; 1.
PR0SITE; PS501357; ZF_ZZ_2; 1.
Zinc_finger; Alternative splicing; Polymorphism.
                                                                                                                                                                                                   send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5, 2004, 09:56:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZZ-TYPE.
UBA.
                                                                                                                                                                                                                                                EMBL; X76952; CAA54274.1; -... EMBL; D30756; BAA06417.1; -... EMBL; BC009808; AAH09808.1; -... EMBL; AF27189; AAF74119.1; -... GMS.744; AAA93228.1; -... GlycountedB; Q14596; -... GlycountedB; Q14596; -... Genew; HGNC:6746; M17S2.
carcinoma antigen CA125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.4%;
85.7%;
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957
714
966
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us-09-761-636a-14.open.rspt

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Q53028
Q53028;
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                                                                                 September 5, 2004, 09:46:09; Search time 20.3636 Seconds (without alignments)
139.448 Million cell updates/sec
                                                                                                                                                                                                                                                                             1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                          1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_human:*
6: sp_mamal:*
7: sp_mhc:*
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sp_unclassified:*
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sp_phage:*
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52
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Maximum DB seq length: 200000000
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17:
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O53028 rhodococcus	O9ma88 arabidopais	P91378 caenorhabdi	Ogzive horrelia hu	ORn2ig homo sanien	Ogney wilells fac	030782 Ajieira ras	Ogunga Arosophila	OSECO COOCHILA	O22243 exellutional	O20243 didbiopsis	Obraha raccus morv	OBSERVE NOME SAPIEM	Obesus money	Openation musculu		
SUMMARIES	ID	Q53028	O9MA88	P91378	9XIZ60	08N7I9			U	096605			C		090731	OBC244	025921	
	DB	7	10	5	~	4		16			10		7	•	11	11	16	
	Query Match Length DB	342	648	362	80	134	154	198	562	568	1015	3623	132	283	287	287	287	
olo.	Query	78.8	76.9	75.0	73.1	73.1	73.1	73.1	73.1	73.1	73.1	73.1	71.2	71.2	71.2	71.2	71.2	
	Score	41	40	39	38	38	38	38	38	38	38	38	37	37	37	37	37	
	Result No.	н	7	'n	4	Ŋ	9	7	<b>c</b> c	6	10	11	12	13	14	15	16	

Q93368 caenorhabdi Q7x9c0 lotus japon 096736 fowl adenov	fuso	Q99y31 streptococc Q8nzf5 streptococc	Q87f37 xylella fas Q8bn56 mis misculu	015716 dictyosteli	Q8n787 homo sapien	O9m7a8 nicotiana t	O86ke8 dictvosteli		Ognby6 homo sapien	Q9ngc0 homo sapien	homo	caenc	O9bpv7 homo sapien		salm	O8zkm1 salmonella		O9bx88 homo sapien		Ogueva strongyloid	S	Q01863 phytophthor
5 Q93368 10 Q7 <b>x</b> 9C0 12 Q96736		_	16 Q87F37 11 Q8BN56	5 015716	4 Q8N787 17 O8TV20	10 Q9M7A8	5 Q86KE8	3 Q9P7Q7	4 QBNBV6	4 Q9NQC0	4 Q86SP2	5 Q9BKR0	4 Q9BPY7	4 Q9BYT4	16 Q8Z306	16 Q8ZKM1	16 Q9PEG0	4 Q9BX88	4 08TDU8	5 Q9U6V3		10 Q01863
407 972 114	147	185	309 442	556	583 650	945	1348	1639	120	143	186	197	249	265	278	283	305	309	388	388	422	496
71.2	01 01 (	69.5	69.2 69.2	69.2	69.7	69.2	69.2	69.2	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3
37 37 36	36	36	36 36	36	3 6	36	36	36	35	32	35	35	35	35	32	32	32	35	35	35	35	35
17 18 19			24 25	26		53	30	31	32	33	34	35	36	37	38	ტ.	40	41	42	43	44	45

### ALIGNMENTS

Saki H., Furuhashi K.;

Sacki H., Furuhashi K.;

"Cloning and characterization of a Nocardia corallina B-276 gene cluster encoding alkene momnoxygenase.";

"Conforms is a constant of the consta Rhodococcus corallinus, Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterineae; Gordoniaceae; Gordonia. NCBI\_TaxID=36822; Last sequence update) Last annotation update) 342 AA. Created) PRT; 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25, Reductase. PRELIMINARY; SEQUENCE FROM N.A. ACCUCATION OF A PACTOR OF A PA

SOW

**Q9MA88** Q9MA88

SO ON SO ON

RESULT 2 Q9MA88

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01-MXY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
4 pypothetical protein.
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria, Spirochaetes; Spirochaetales; Spirochaetales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ25492.
Homo sapiens (Human)
Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                           DB 5; Length 362;
29;
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Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRANIB-N40;
Fong S., Chen G., Barthold S.;
"G5 clone from Borrelia burgdorferi.";
Submitred (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF0050565; AAD01230.1;
Hypothetical protein.
                                               "The sequence of C. elegans cosmid K12D9.";
submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                             Waterston R.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                        Wilson R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                           F25CFD3B0E1D9435 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C61A1E359DED8EA3 CRC64;
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                                                                                                                                                                                                                                                                                                                                           Score 39; DB 5; Pred. No. 29; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                             362 AA; 41292 MW;
                                                                                                                                                                                                                                                                                                                                               75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.1%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9171 MW;
                                                                                                                                                                                                                                                                          EMBL; U80030; AAG24161.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 CISLPIVIC 241
                                                                                                                                                                                                                                                                                                                                                                                                                     1 CISVPLVPC 9
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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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TISSUE=Brain;
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                                                                                                          SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=Bristol N2;
SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                    Graves T.;
"The sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=139;
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
112H1.28 protein.
112H1.28 thaliana (Mouse-ear cress).
12H1.28 thaliana (Mouse-ear cress).
12H1.28 protein.
12H1.28 thaliana (Mouse-ear cress).
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T12H1 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ACC09377; AAF27037.1; -.
GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IRR002048; EF-hand.
PROSITE; PS00018; EF-hand.
PROSITE; PS00018; EF-HAND; 2.
SEQUENCE 648 AA; 73066 MW; D22FD23B724DBB7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                            Length 342;
                                                                                                                Indels
                                        342 AA; 37282 MW; 4651F38D116A8049 CRC64;
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                                                                            78.8%; Score 41; DB 2; 77.8%; Pred. No. 11; tive 0; Mismatches
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     PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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01-NAY-1997 (TrEMBLrel. 03,
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
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Matches 6; Conservative
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                                                                                                 Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                      75 CASVPLEPC
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SEQUENCE FROM N.A.
                          Iron; Iron-sulfur
SEQUENCE 342 AA.
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Alwarenga R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S.,
Alwarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Alwarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Borddin S., Bove U.M., Friones M.R.S.,
Bueno W.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa-Neto C.M.,
Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Fraga J.S., Franca C.C., Franco M.C., Frohme M., Furlan L.R.,
A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
Rrieger J.E., Kuramae B.E., Laigref F. Lambais M.R., Leite L.C.C.,
A Krieger J.E., Martins E.A.L., Martins C.L.,
Machado M.A., Madelira A.M.B.N., Madelira H.M.F., Markou C.L.,
Marques M.V., Mardins E.A.L., Mathins E.M.P., Markou C.L.,
Marques M.V., Mardins E.A.L., Mathins E.M.P., Marsukuma A.Y.,
Mardins A. Jr., Nobrega F.G., Miyaki C.Y., Monteiro-Vitorello C.B.,
Mhani A. Jr., Nobrega F.G., Miyaki C.Y., Monteiro-Vitorello C.B.,
Man A. Jr., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
Colyuggio R.B., Poberto P.G., Rodrigues V., de Rosa A.J.M.,
de Rosa V.B. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A de Silve A.C.R., da Silva A.M., da Silva F.R., Silva W.J.,
A de Silva A.C.R., da Silva A.M., Verjovski-Almeida S., Vettore A.L.,
A Sago M.A., Zatra M., Meidadianis J., Setubal J. C.,
A Sago M.A., Zatra M., Meidadianis J., Setubal J. C.,
A Sago M.A., Zatra M., Pariadianis J., Setubal J. C.,
A Sago M.A., Zatra M., Pariadianis J., Setubal J. C.,
A Sago M.A., Zatra M., Pariadianis J., Setubal J. C.,
A Sago M.A., Zatra M., Pariadianis J., Setubal J. C.,
A Sago M.A., Zatra M. Pariadianis J., Setubal J. C.,
A Sago M.A., Zatra M. P. L. Sawasaki H.S.
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Nishi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M. Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., Nagai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome sequence of the plant pathogen Xylella fastidiosa.";
Nature 406:151-159(2000)
EMBL; AE003900; AAF83323.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                      .
                                                                                                                                                                                                4; Length 134;
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                                                                                                                                   Hypothetical protein.
SEQUENCE 134 AA; 13911 MW; 9605A9F9912C2802 CRC64;
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Last sequence update)
Last annotation update)
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GO: 00:00016998; P:cell wall catabolism; IEA.
GO; GO:0009253; P:peptidoglycan catabolism; IEA.
InterPro; IPR002196; Glyco_hydro_24.
Pfam; PF00959; Phage_lysozyme; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           154 AA
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MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                73.18;
77.88;
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01-0CT-2000 (TrEMBLrel. 15,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                              Local Similarity 77.8
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SEQUENCE 154 AA
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Bannantine J.P., Rockey D.D., Hackstadt T.;
"Tandem genes of Chlamydia psittaci that encode proteins localized to
                                             Gaps
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Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae.";
                                                                                                                                                                                                                                                                                                                                                               Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Bhydroidea; Drosophilidae; Drosophila, NCBI_TaxID=7227;
        DB 16; Length 154;
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                                               Indels
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                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                            198 AA.
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                                             2; Mismatches
        Score 38;
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EMBL; AF017105; AAC46378.1; -.
EMBL; AE016995; AAP05235.1; -.
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                                                                                                                                                                                                                                                                                                                           Inclusion membrane protein B.
    73.1%;
75.0%;
Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity
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                                                                                   1 CISVPLVP
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SEQUENCE 198 AA
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MEDLINE=20083487; PubMed=10617197; MEDLINE=20083487; PubMed=10617197; MEDLINE=20083487; PubMed=10617197; MEDLINE=20083487; Pubmed=10., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                     73.1%; Score 38; DB 5; Length 568; 66.7%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                          STRAIN=Bristol N2;
Cordes M., Wohldmann P.;
"The sequence of C. elegans cosmid Y24D9A.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                       Waterston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
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GO; GO:0008026; F:ATP dependent helicase activity; IEA.
GO; GO:0016787; F:Hydrolase activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                              SMART; SM00317; SET; 1.
PROSITE; PS50280; SET; 1.
Hypothetical protein.
SEQUENCE 568 Aa; 65908 MW; EE4299BIDCFBE98D CRC64;
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(TrEMBLrel. 11, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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 investigating biology. The C
Science 282:2012-2018(1998).
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WormPep; Y24D9A.2; CE33849.
InterPro; IPR001214; SET.
Pfam; PF00856; SET; 1.
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Best Local Similarity 66...
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                                                         SEQUENCE FROM N.A.
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01-JAN-1998
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                                                 Adams M.D. (Celliker S.E. ii P.W. Hoskins R.A., Gocayne J.D., RAMEDLINES-198606; FubMed=10718.X. Adams M.D. (Celliker S.E. ii P.W. Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Ii P.W. Hoskins R.A., Galle R.E., Gocoge R.A., Elevis S.E., Scherer S.E., ii P.W. Hoskins R.A., Galle R.D., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Sutton G.C., Bazdwin D.A., Bardon R.R., Malson C.R., Miklos G.L.G., Ram M.H., Doyle C., Bazdwin A., An H.-J., Andrews-Febrankoch C., Baldwin D., Ballew R.M., Basu A., Barenan B.P., Bhandari D., Bolshakov S., Ballew R.M., Dayle C., Bosen D.W., Ewendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Cawley S., Daller H., Cadteu E., Center A., Chandra I., Burtis R.C., Busan D.A., Deng Z., Mays A.D., Dew I., Dietz S.M., Rockery S., Dallocher A., Long Z., Mays A.D., Dew I., Detz S.M., Re Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Achtery D., Harvey D., Hernandez J.R., Bourk B., Durkow B.C., Dunn P., Durbin K.J. Evangelista C.C., Ferriaz C., Guar P., Harris M., Goog F. Correll J.H., Gals C., Genar W., Goog F. Correll J.H., Gals C., Gann R.A., Hawland T.J., Hernandez J.R., Houck J., Hould M., Harvey D., Hennandez J.R., Houck J., Hould J. A., Alalali M., Kalush F., Karatiz S., Kulp D., Lai Z., Alalali M., Kalush F., Karatiz S., Kulp D., Lai Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., R. Melson D.L., Mourt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nathy D., Murshell D.K., Baller M., Moy M., Murphy B., Wurshell M., Scheeler F., Shen H., Spier E., Spradling A.C., Stapheton M., Skupski M.P., Shen H., Spier E., Spradling A.C., Thurshell M., Scheeler F., Shen B., Spier E., Spradling A.C., Stapheton M., Stupski M., Stup S., Thu X., Wang Z.-Y., Wasserman D.A., Wainstock G.M., Weissenbach J., Wang Z.-Y., Wasserman D.A., Wainstock G.M., Weissenbach J., Yeb R., Weissenbach J., Schoeler T., Worley K., Wu D., Yang S., Zhoo S., Zhoo S., Zhoo S., Zhoo S., Zhoo S., Zho
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI TaxID=6239;
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Last annotation update)
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2; Mismatches
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MEDLINE=99069613; PubMed=9851916;
Wilson R.;
                                         MEDLINE=20196006; PubMed=10731132;
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01-CCT-2003 (TrEMBLrel. 25, La
Hypothetical protein Y24D9A.2.
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TISSUE=Phyroid;
Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
Ninomiya K., Wagatsuma M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
Kateuta N., Saco K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
Nakagawa K., Otsuki T., Sato H., Nishikawa T., Sugiyama T.,
Nagai K., Isogai T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO98419; BACOS303.1; --
Hypothetical protein.
SEQUENCE 132 AA; 14716 MW; 8C2661CAOEB7309B CRC64;
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.2%; Score 37; DB 4; Length 132; 62.5%; Pred. No. 26; ative 3; Mismatches 0; Indels
                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FL725553.
Homo sapiens (Human).
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Best Local Similarity 62.53,
Than 5; Conservative
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SEQUENCE
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Q86SUS;
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Masmussen H.H., Brault D., Pontillon F., Goda F.O., Christensen E.I.,

Hasmussen H.H., Brault D., Pontillon F., Goda F.O., Christensen E.I.,

Hammond T.G., Verroust P.J.;

The intrinsic factor-vitamin Blz receptor and target of teratogenic

The intrinsic factor-vitamin Blz receptor and target of teratogenic

The intrinsic factor-vitamin Blz receptor and target of teratogenic

The intrinsic factor-vitamin Blz receptor and target of teratogenic

The intrinsic factor-vitamin Blz receptor and target of teratogenic

The intrinsic factor-vitamin Blz receptor and target of teratogenic

The monloy to developmental proteins ";

J. Biol. Chem. 273:5235-5242(1998).

E. J. Biol. Chem. 273:5235-5242(1998).

E. J. Biol. Chem. 273:5235-5242(1998).

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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CHAIN 21 3623 INTRINSIC FACTOR-B12 RECEPTOR.
SEQUENCE 3623 AA; 398981 MW; 39FB792AC6545240 CRC64;
                                                       SWART; SW00487; DEXDC; 1.
SWART; SW00490; HELICC; 1.
SWART; SM00356; ZnF C3H1; 2.
ATP-binding; Helicae; Hydrolase.
SEQUENCE 1015 AA; 115084 MW; D1C342B338C561C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 3623 AA.
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Pfam; PF00008; EGF; 5.
SMART; SM001042; CUB; 26.
SMART; SM0179; EGF CA; 4.
PROSITE; PS00110; ASX HYPROXYL; 3.
PROSITE; PS01180; CUB; 27.
PROSITE; PS01180; CUB; 27.
PROSITE; PS01180; EGF 2; 2.
PROSITE; PS01187; EGF 2; 2.
PROSITE; PS01187; EGF CA; 4.
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MEDLINE=98148073; PubMed=9478979;
                   Pfam; PF00271; helicase C; 1.
Pfam; PF00642; zf-CCCH; 2.
InterPro; IPR000571; Znf
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Matches 6; Conservative
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                                                                                                                                                         Query Match
Best Local Similarity
6; Conserve
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE FROM N.A.
TISSUB-Lung, Spleen, and Fetal;
Strausberg R.;
L Submitted (DEC 2002) to the EMBL/GenBank/DDBJ databases.
R Genew; HGRO(18411, SAN13.
R GO; 00005507, F.copper ion binding; IEA.
R GO; 00005507, F.copper ion binding; IEA.
R InterPro; IPR007087; Znf CZH2; S.
R Pfam; PF000096; Znf CZH2; 1.
R Probom; PD000003; Znf CZH2; 1.
R Probom; PD0000035; Znf CZH2; 1.
R SMART; SM00355; Znf CZH2; 1.
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                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to snail homolog 3 (Drosophila) (Fragment).
                                                                                                                                                                        283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00080; MULTCOPPER OXIDASE2; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
                                                                                                                                                                        PRT;
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121 LAVPLIPC 128
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Best Local Similarity
Matches 6; Conserv
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313 ČSQAPĽVPC 321

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1 CISVPLVPC 9

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Search completed: September 5, 2004, 10:00:09 Job time: 22.3636 secs
                                              STRAIN=NOD
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                                                                                                                                                                  Kataoka H., Murayama T., Yokode M., Mori S., Sano H., Ozaki H.,
Yokota Y., Nishikawa S.I., Kita T.;
"A novel Snail-related transcription factor Smuc regulates basic
motifs.loop-helix transcription factor activities via specific B-box
motifs.";
                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                               Q9QY31;
01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Snail-related zinc finger protein SWUC (Zinc finger protein 293).
SNAI3 OR ZFP293 OR SWUC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 75.0%; Pred. No. 54; Gonservative 2; Mismatches 0; Indels
                                                        287 AA
                                                                                                                                                                                                                 Nucleic Acids Res. 28:626-633(2000).
                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=B6;
MEDLINE=20075155; PubMed=10606664;
                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8C244, PRELIMINARY;
Q8C244,
01-MAR-2003 (TrEMBLrel. 23, C1
01-MAR-2003 (TrEMBLrel. 23, La
01-CT-2003 (TrEMBLrel. 25, La
Zinc finger protein 293.
                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 CISLPLLP 74
         |||:||:|
58 CISLPLLP 65
                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CISVPLVP 8
 8
 1 CISVPLVP
                                                                                                                                  NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                       Q9QY31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                        RESULT 14
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Created)
Last sequence update)
Last annotation update)

SELTER S

287 AA

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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                           R MGD; MGI:1353563; Brad:3.

R MGD; MGI:1353563; Brad:3.

R GO; GO:0005667; C:transcription factor complex; IDA.

GO; GO:000300; F:transcription of transcription, DNA-dependent; IDA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.

InterPro; IPR000345; Cu_ox_copper_BS.

InterPro; IPR000345; CytC_heme_BS.

R InterPro; IPR000347; Zhf_C2H2.

R ProDom; PO000063; Zhf_C2H2.

R PROSITE; PS000190; CYTOCHROME C; 1.

R PROSITE; PS000190; CYTOCHROME C; 1.

R PROSITE; PS000080; MIC_INGER_CZH2.1; 4.

R PROSITE; PS000080; ZINC_FINGER_CZH2.1; 4.

R PROSITE; PS00197; ZINC_FINGER_CZH2.1; 4.
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Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.2%; Score 37; DB 11; ilarity 75.0%; Pred. No. 54; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AK089285; BAC40828.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 6; Conserv
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                          NCBI_TaxID=10090;
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2004, 09:37:49; Search time 29.5455 Seconds (without alignments) 86.068 Million cell updates/sec
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                           protein search, using sw model
                                                                                            ď,
                Copyright
                                                                                            September
                                                              ı
                                                           OM protein
                                                                                          Run on:
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Title: Perfect score:

US-09-761-636A-14 52 1 CISVPLVPC 9 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\*
geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* geneseqp1980s:\* geneseqp2004s:\* .. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ユー・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・	1000	TOEVE S	Noon			· N		Nove		,				١ ٩				Zinc f					Nove		
SUMMARIES	ID	AAU04533	AAU04532	AAU04526	AAR66216	AAR81472	AAU04545	AAU04542	AAM06501	ABG22400	ABP77742	AAY27025	AAY32174	ADB64366	ABB57779	ADA35614	AAY27020	AAG00458	AAY12860	AA016348	ABU96694	ADA55489	AAU04544	ABP28862	AAW85729	ADC38773	
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æ	Query Match	100.0	79.8	78.8	78.8	78.8	76.9	LO.	75.0	75.0	75.0	73.1	73.1	73.1	73.1	73.1	73.1	71.2		71.2	71.2	71.2	69.2	69.2	67.3	67.3	
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Aam93613 Human pol Abg03676 Novel hum	Aaw79090 Human sec Aau12226 Human DBO	Human	Humar	Humar	Abol7670 Novel hum	Humar	Nove	Human	Human		Ada45629 Novel him	Human	Human	Homo	Nove	Human
4 AAM93613 4 ABG03676	2 AAW79090 4 AAU12226	~.	5 AAM49039	-	6 ABUI/6/U				6 ABU66900	6 ABP54449	6 ADA45629	6 ADA76060	6 ADA18710	6 ADA61333	6 ADB19118	6 ADB27659
120	249 249	249	249	647	24.9	249	249	249				-	_	249	249	249 (
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26	7 7 7 8 7 8	30	3. 1.	א ה א ר	3.5	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. Location/Qualifiers 1. .9 /note= "This bond cyclises the peptide" Cendron A; Stacker S, VEGF based monocyclic peptide 11. AAU04533 standard; peptide; 9 AA. (LUDW-) LUDWIG INST CANCER RES. 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533. (first entry) Hughes RA, WPI; 2001-442248/47. Key Disulfide-bond WO200152875-A1. 26-SEP-2001 26-JUL-2001. Synthetic. Achen MG, AAU04533; 

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues. Novel

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a residues.

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peptide loop tragment from an exposed loop of a glownin raccol, process, or cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides with at least one amino acid deleted prior peptides) and a cyclic peptide with at least one amino acid deleted prior concition are used to interfere with angiogenesis. The monocyclic neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, head, head or cold crampional, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability or brain. The peptides are used to image blood vessels and lymphatic cor brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to inferfere with at least one biological activity induced by VEGF. VEGF-C or -D and care also used in combination with an anti-inflammatory agent, to treat a continion inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
peptide loop fragment from an exposed loop of a growth factor protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
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    10
/note= "This bond cyclises the peptide"

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100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU04532 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9 AA;
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human construction relates to a method of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis.

CC cyclisation are used to interfere with angiogenesis.

CC corolisation are used to interfere with angiogenesis.

CC corolisation is diabeted retinopathy, peoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold craums, substance-induced neovascularisation or lymphanglogenesis.

CC fraums, substance-induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver confiction. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition diabetes induced neovascular communitation in peripheral limbs or in lungs, peritoneal carbity, pleura, or brain. The peptides are used to indeptides are used to indeptice or brain. The peptides are used to indeptides are used to indeptive or brain. The peptides are used to indeptides are used to indeptive or brain at least one biological activity induced by VEGF, VEGF-C or D and chronic inflammation are permeability in hemmatical archival archivity services and chronic inflammation archival archival archivity services and and archivity induced by VEGF, VEGF-C or D and chronic inflammation and priorice and archivity induced archivity induced archival archival and archivity induced archival and archivity induced archival archival and archivity induced archivity induced archival 
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Pred. No. 2.2;
0; Mismatches 0; Indels

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/note= "This bond cyclises the peptide"

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                                     Claim 49; Page 32; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEGF based monocyclic peptide 3.
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16-MAY-2000; 2000US-0204590P.
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Best Local Similarity 90.v
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06-APR-1993;
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                                                                                                                                                                                                                 The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vibose 3-dimensional structure is modelled on the expose loop of human viboric dearbon separation distances on opposite antiparallel strands of a beta-beta carbon separation distances on opposite antiparallel strands of a cyclising the peptide by exidising the cystein ersidues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid delated prior or cyclisation are used to interfere with angiogenesis.

CC cordisation are used to interfere with angiogenesis.

CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC crebrovascular accident, post-angioplasty restenosis, head, heat or cold crauma substance-induced neovascularisation of the liver, excessive correction. The peptides are also used to modulate vascular permeability and mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, ovasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. Core or and and are also used to interfere with at least one biological activity induced by versulation in combination with an anti-inflammatory agent, to treat a diabetic resident residual activity induced by VEGF. Core or and and activity induced activity seriasis and characterises and correction in the periode are also used to interfere and correction and activity induced by VEGF. Core or band are also used in combination with an anti-inflammatory agent, to treat a diabetic residual activity.
                                                                                                    Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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                                        Cendron A;
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Pred. No. 2.9;
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                                                                                                                                                                                             Claim 49; Page 32; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR66216 standard; protein; 342 AA.
                                        Stacker S,
   (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.8%;
81.8%;
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                                      Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
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CISVPLTSVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CISVPL--VPC
                                                                       WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP06292571-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2003
04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-OCT-1994
                                    Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR66216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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                                                                                                                     Alkene mon:oxygenase and corresp. gene - useful for the epoxidation of an
                                                                                                                                                                                                      E.coli transformed with the DNA sequence AAQ79569 are able to catalyse the epoxidation of alkenes. The DNA is derived from Nocardia corallina and comprises 4 open reading frames. ORFs amoA and amoC encode subunits 1 and 2 of the alkene monoxygenase enzyme and ORF amoD encodes a reductase capable of transferring electrons from NADH coenzyme to a monoxygenase. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR81469-R81472 are protein products of the Nocardia corallina strain B-276 alkene mono-oxygenase gene. The gene encodes 4 protein products amoh, amoB, amoC and amoD derived from the 3 different reading frames of the operon. The gene is useful for the production of indigo via oxidation of indole. Nocardia corallina can be cultured in a medium cong. indole and will readily oxidise the indole yielding indigo into the culture medium. E. coli may also be transformed with the alkene mono-oxygenase gene and (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prepn. of indigo by a microbiological method - by culturing a microbe having alkene monoxigenase activity to oxidise indole to indigo.
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alkene mono-oxygenase; indole; indigo production; biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nocardia corallina alkene mono-oxygenase gene product, amoD.
                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 2; Length 342;
Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR81472 standard; protein; 342 AA.
                                                                                                                                                                         Claim 2; Page 4-5; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 8-9; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gordonia rubripertinctus; B-276.
93JP-00105171
                                                                                                                                                                                                                                                                                                                                                                          78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94JP-00179688
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                             (NIHA ) JAPAN ENERGY CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 7/...
7/...
7/. Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microbial oxidation; dye.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                 WPI; 1995-009069/02.
N-PSDB; AAQ79569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-133426/14.
N-PSDB; AAT17418.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CISVPLVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CASVPLEPC
                                                                                                                                                                                                                                                                                                                                     Sequence 342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP08023988-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2003
07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR81472;
                                                                                                                                         alkene.
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RESULT 7
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                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human converse of vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betact carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides, dimeric blcyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

To cyclisation are used to interfere with angiogenesis.

To cyclisation or lymphangiogenesis in a mammal with a condition convacularisation or lymphangiogenesis. Necessity the condition is diabetic retinopathy, psoriasis, arthropathy convergences or condition accident, post-angioplasty restences; head, heat or cold cramancioma, vascularised malignant or benign tumour, post-recovery creamens, substance-induced neovascularisation of the liver, excessive chrama, substance-induced neovascular sequelae, or chronic liver sequelar.
                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                               Gaps
                                                                                                                                                                                                                                                                   Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                               ö
                                       Length 342;
                                                               2; Indels

    .11
/note= "This bond cyclises the peptide"

                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cendron A;
                                                   86;
                                                                Mismatches
                                        Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stacker S,
                                                                                                                                                                         AAU04545 standard; peptide; 11 AA
                                                                                                                                                                                                                                               VEGF based monocyclic peptide 23.
                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2001; 2001WO-US001533
                                       78.8%;
77.8%;
                                                                                                                                                                                                                         26-SEP-2001 (first entry)
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hughes RA,
                                                                                                            CASVPLEPC 83
                                                                                       CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-442248/47.
                                       Query Match
Best Local Similarity
Matches 7; Conserv
                 Sequence 342 AA;
                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                         WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Achen MG,
                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                  AAU04545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residues.
                                                                                        Н
                                                                                                               75
                                                                                                                                                     RESULT 6
                                                                                                                                                                AAU04545
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                                                                                                               qq
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vEGFD (vascular endothellal growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
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in fection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 4; Length 11; Pred. No. 4.2; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU04542 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF based monocyclic peptide 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                 76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                               72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 72.7
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVSVPLTTVPC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CISVPL--VPC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                    Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU04542;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or crauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and chronic inflammation, especially rheumatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and riabetic retinoral periodes.
cyclisation are used to interfere with angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetic retinopathy
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Sequence 11 AA;

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Gaps
                                    5,
 75.0%; Score 39; DB 4; Length 11; 72.7%; Pred. No. 6.2; 0; Indels ive 1; Mismatches 0; Indels
                               Conservative
                                                         1 CISVPL--VPC 9
             Local Similarity
nes 8; Conserv
Query Match
                            Matches
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CLSVPLTSVPC 11

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AAM06501 standard; protein; 101 AA. RESULT

(first entry) 05-OCT-2001 AAM06501;

Human foetal protein, SEQ ID NO: 232.

Human; foetal protein; cytostatic; immunosuppressive; immunostimulant; nootropic; neuroprotective; thrombolytic; osteopathic; antiinflammatory; gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder; nervous system disorder; inflammation. 

Homo sapiens

WO200155339-A2

02-AUG-2001

25-JAN-2001; 2001WO-US002723

2000US-00491404 2000US-00663870 25-JAN-2000; 2000US-00491404 15-SEP-2000; 2000US-00663870 06-NOV-2000; 2000US-00707351

HYSEQ INC. HASE-)

Tang YT; Drmanac RA, Boyle BJ, Arterburn MC, Zhou P, Werhman T; Ford JE, Asundi V, Yeung G, Liu C, A

WPI; 2001-465571/50. N-PSDB, AAH94176. Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune disorders, growth disorders, thrombolytic disorders, nervous system disorders and inflammation.

Claim 10; Page 264; 715pp; English.

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The invention relates to novel foetal polypeptides encoded by polymuclectides comprising one of 477 sequences fully defined in the specification. The foetal polymuclectides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present sequence is a polypeptide encoded by a cDNA assembled using an expressed sequence tag (EST) found to be expressed in human foetal tissue cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a bolypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                          Score 39; DB 4; Length 101;
Pred. No. 55;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 52759; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #22391.
                                                                                                                                                                                                                                                                                                                                                                                                               ABG22400 standard; protein; 102 AA.
                                                                                                                                                                                                          75.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-00540217
2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                     Query Match
Best Local Similarity
7; Conserv?
                                                                                                                                                                                                                                                                                    α
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                                                                                                                                                                                                                                                                                1 CISVPLVP
                                                                                                                                                                                                                                                                                                                    2 CISVPLTP
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                                                                                                                                                                      Sequence 101 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity.
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AAY27025 standard; protein; 44 AA.
                                             AAY27025;
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0
and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and cantibodias that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABPP6736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               manufacture of
                                                                                                                                                                    Gaps
                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n from Neisseria gonorrheae, useful for the manufact
for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 6; Length 347;
Pred. No. 1.9e+02;
2; Mismatches 0; Indels
                                                                                                                                      DB 4; Length 102;
                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Antibacterial; infection; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                               N. gonorrhoeae amino acid sequence SEQ ID 2014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>й</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monaci
                                                                                                                                                    Pred. No. 56;
                                                                                                                                        Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New protein from Neisseria gonorrheae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 334; 815pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Masignani V,
                                                                                                                                                                                                                                                                                                       ABP77742 standard; protein; 347 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-2002; 2002WO-IB002069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-2001; 2001GB-00003424
                                                                                                                                        75.0%;
                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75...
6; Conservative
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fontana MR, Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria gonorrhoeae
                                                                                                                                                                                                                              24 CFSVPLVP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-058415/05.
                                                                                                                                                                                                   1 CISVPLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR-) CHIRON SPA
                                                                                                                                        Ouery Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABZ38712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 347 AA;
                                                                                                           Sequence 102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200279243-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  medicament
                                                                                                                                                                                                                                                                                                                                     ABP77742;
                                                                                                                                                                                                                                                                            RESULT 10
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The invention relates to a rat cubilin protein. Cubilin is a ligand-
binding, epithelial glycoprotein receptor that facilitates uptake of
intrinsic factor/vitamin B12 complexes in intestines and Kidney. It is
also involved in endocytosis and trafficking of light immunoglobulin
claims in renal proximal tubule cells. Host cells containing a vector
comprising the rat cubilin DNA sequence can be used for the recombinant
expression of the protein. Cubilin, or its fragments, are used to treat
or reduce toxicity, particularly in Kidneys, spheen, brain, liver, heart
and thyroid. Cubulin mutations may also be implicated in idiopathic
proteinuria, fetal malformation, poor fetal development and spontaneous
proteinuria, fetal malformation, poor fetal development and spontaneous
proteinuria, fetal malformation, poor fetal development and spontaneous
contist detection, or clones that express it, in standard immunoassays.
Fragments of cubilin DNA can also be used to detect cubulin mRNA in cell
and tissues, by hybridization. Abnormal levels of cubilin in the urine
are indicative of kidney damage. Sequences ANY27021-35 represent EGF
repeat sequences of rat cubilin and from homologous regions of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·.
                                                                                                Cubilin; epithelial glycoprotein receptor; vitamin B12; endocytosis; toxicity; kidney; spleen; brain; liver; heart; thyroid; abortion; rat; proteinuria; fetal malformation; fetal development; kidney damage; BGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA encoding cubilin, used for treating toxicity, particularly nephrotoxicity, and as marker of kidney damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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ص
                                                   Amino acid sequence of rat cubilin EGFS repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TULA ) TULANE EDUCATIONAL FUND.
(INRM ) INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY32174 standard; protein; 198 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 18; Fig 6A; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US001259.
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(first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Verroust PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 CSQAPLVPC 20
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 44 AA;
                                                                                                                                                                                                                                                                                          W09937757-A1
                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-1999;
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01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hammond TG,
   08-OCT-1999
                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999.
                                                                                                                                                                                                                                       Rattus sp.
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RESULT 11

CISVPLVP 8

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The invention discloses a polynuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel colypeptides. Also claimed is a polypeptide encoded by the polynuclectide or its partial peptide, an antibody binding to the polypeptide or peptide or peptide of the polynuclectide by contacting the polypeptide or peptide or peptide by contacting the polypeptide or peptide or peptide by contacting the polypeptide or peptide or the polynuclectide by contacting the polypeptide or peptide or peptide between the two, a transformant carrying the polypuclectide in an expressible manner and an antisense polynuclectide. The oligonuclectide is useful as a primer for synthesising the polynuclectide and encoded or contacting the polynuclectide. The polynuclectide and encoded or proteins are useful as pharmaceutical agents and many disease-related genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets or genes therapy. The genes are involved in tissue and/or cell credencation. Membrane proteins, signal transduction-related proteins, correctine the activity or expression of the encoded proteins and genes or encoding them can be used as indicators for diseases (e.g. osteoporosis, the activity or expression of the encoded protein to treat diseases. The correct presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed correction of the correction of the invention supplied by the correction of the correction of the invention supplied by the correction of the invention supplied by the correction of the invention of the printed information supplied by the correction of the invention of the printed information supplied by the correction of the invention of the invention of the correction o
                                                                                                                                                                                                                                                      Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotides and polypeptides, useful for developing a diagnostic ter or medicines for regulation of their expression and activity, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB57779 standard; protein; 562 AA.
                                                                                                                                                                        (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page; 222pp; English.
                                             28-MAR-2002; 2002EP-00007401
                                                                                                05-NOV-2001; 2001JP-00379298
                                                                                                                        25-JAN-2002; 2002US-00350978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as targets of gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                   Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 CASLPLSPC 41
                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-450961/43.
N-PSDB; ADB62396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                               marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents novel infection-specific protein IncB of chlamydia psittaci strain GPIC. IncB is found in the inclusion membrane of infected cells. It is associated primarily with the vegetative reticulate body form of Chlamydia rather than with the refractile elementary body form. The invention includes: a vaccine directed against the reticulate body form of Chlamydia comprising 1 or more infection-specific proteins (see AAY3170-78), including IncA, IncB and IncC; methods of using and producing such a vaccine; methods for detection of methods of using therapeutic agents specifically directed against infection-specific antibodies or antigens in a biological specimen; and a method of using therapeutic agents specifically directed against infection-specific peptides, or the genes that code for such peptides, to real chlamydial infection. (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, pharmaceutical, diagnostic, gene therapy, tissue regeneration,
cell regeneration, membrane protein, signal transduction-related protein,
transcription-related protein, osteoporosis, neurological disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel bacterial infection specific proteins for treating and diagnosing
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Chlamydia psittaci infection-specific protein IncB.
                                                     IncB; infection; vaccine; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein encoded by clone FCBBF30171230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 41-42; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB64366 standard; protein; 208 AA.
                                                                                                                                                                                                                                                                                                              98US-0082438P.
98US-0082588P.
98US-0086450P.
                                                                                                                                                                                                                                                                 99WO-US008744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rockey DD, Bannantine JP;
                                                                                                                                                                                                                                                                                                                                                                                                                 (UYOR-) UNIV OREGON STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chlamydial infections
                                                                                                        Chlamydophila caviae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-633904/54.
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Best Local Similarity
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                                                                                                                                                        WO9953948-A1
                                                                                                                                                                                                                                                                                                                                         21-APR-1998;
22-MAY-1998;
                                                                                                                                                                                                                                                                 20-APR-1999;
                                                                                                                                                                                                                                                                                                                 20-APR-1998;
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field)

Matches

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Gaps

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Score 38; DB 7; Length 208; Pred. No. 1.6e+02; 1; Mismatches 2; Indels

1; Mismatches

Drosophila, developmental biology, cell signalling, insecticide,

Drosophila melanogaster.

pharmaceutical

Homo sapiens EP1308459-A2

ADB64366;

07-MAY-2003.

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N-PSDB; ADA31488
                           RESULT 15
                           ADA35614
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New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                   The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 6; Length 589;
Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: September 5, 2004, 09:55:23 Job time : 31.5455 secs
                                                                                                                                 Example; SEQ ID NO 6901; 328pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.1%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          273 CISVPLFHC 281
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                                                                                                                                                                                                                                                                                                                                                                    baumannii protein
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 589 AA;
                                                                                       plants.
q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7137-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 129; 21pp + Sequence Listing; English.
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Pred. No. 4.4e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                           Li PWD, Myers EW;
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                                                                                            23-MAR-2001; 2001WO-US009231.
                                                                                                                                      23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75
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WO200171042-A2
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Gaps

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1298764 seqs, 315065143 residues
                                                                                                                    OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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52
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Semience 14. April	Sequence 13. Ar	Semience 7 Appl	. ~	Sequence 23. Appl	Sequence 181998	Segmence 2520	Semience 519 Arr	Semience 258586	Semience 165772	Semience 158427	Semience 3057 an	Semience 25 Appl	Segmence 148570	Sequence 279501
SUMMARIES	QI	US-09-761-636A-14	US-09-761-636A-13	US-09-761-636A-7	US-09-761-636A-26	US-09-761-636A-23	US-10-437-963-181998	US-10-104-047-2520	US-10-087-192-519	US-10-424-599-258586	US-10-424-599-165772	US-10-424-599-158427	US-10-094-749-3057	US-09-761-636A-25	US-10-437-963-148570	US-10-424-599-279501
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### ALIGNMENTS

US-09-761-636A-14

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Gaps
                                                        APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REPERBROKE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PLING DATE: 2000-01-18
PRIOR PAPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 14
SEQ ID NO 14
SEQ ID NO 14
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Sequence 14, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Matches 9, Conser
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RESULT 2 US-09-761-636A-13 Sequence 13, Application US/09761636A Patent No. US20020065218A1

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Gaps

2;

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APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad TITLE OF INVENTION: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STACKER, Steven
APPLICANT: FUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, ADER
TITLE OF INVENTION: VEGE-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE REFERENCE: 1064/46505 Achen et al
FILER REFERENCE: 1064/46505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR PRILING DATE: 2000-01-18
PRIOR PRILING DATE: 2000-01-18
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR FILE REFERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: US/09/761,636A CURRENT FILING DATE: 2001-01-18 PRIOR FILING DATE: 2000-01-18 PRIOR FILING DATE: 2000-01-18 PRIOR PILING DATE: 2000-01-18 PRIOR PILING DATE: 2000-05-16 NUMBER OF SEQ ID NOS: 34 SOFTWARE: Patentin version 3.0 SEQ ID NO 26 LENGTH: 11
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Pred. No. 5;
1; Mismatches
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zao, Yihua
APPLICANT: Gao, Yihua
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-761-636A-23
'Sequence 23, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
APPLICANT: ACHEN, MAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: synthetic construct
US-09-761-636A-23
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-26
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Best Local Similarity
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Sequence 7, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:
APPLICANT: ACHEN, MAXC

APPLICANT: STACKER, Steven

APPLICANT: CENDROW, Angela

TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFREENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT FILING DATE: 2001-01-18

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Version 3.0
                                          APPLICANT: ACHEM, MARC
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: GENERAL PRICHARD
APPLICANT: CENDROW, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2000-01-01-8
PRIOR PILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR PILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41.5; DB 9; Length 10;
Pred. No. 2.6;
0; Mismatches 0; Indels
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Best Local Similarity 81.8%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches (
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US-09-761-636A-26
i Sequence 26, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
    APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.8%;
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Best Local Similarity 90.0.
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                           GENERAL INFORMATION:
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US-09-761-636A-7
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TYPE: PRT

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FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 181998
LENGTH: 71
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; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESERRCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.1%; Score 38; DB 15; Length 208; 66.7%; Pred. No. 1.7e+02; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                     75.0%; Score 39; DB 16; Length 71; 62.5%; Pred. No. 42; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1919, Application US/10087192
Sequence 1919, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/7947,377
PRIOR FILING DATE: 2000-10-03-01
PRIOR FILING DATE: 2000-10-03-01
SPRIOR FILING DATE: 2001-03-02
SOUTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 519
                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_79226C.1.pep
US-10-437-963-181998
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Matches 5, Conservative
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                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Mus musculus
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57 CLSIPLIP 64
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Best Local Similarity
Matches 6; Conserv
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US-10-104-047-2520
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LENGTH: 208
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APPLICANT: La Rosa Thomas J
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihuua
APPLICANT: Zhou Yihuua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE REPERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 165772
LENGTH: 94
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COTHER INFORMATION: Clone ID: PAT_MRT3847_120707C.1.pep
US-10-424-599-165772
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US-10-424-599-258586
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66.7%; Pred. No. 3.2e+02;
tive 0; Mismatches 3;
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OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(413)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-087-192-519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 258586, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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69 CLSIQLTPC 77
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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Matches 5; Conserv
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NAME/KEY: unsure
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buchkarov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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APPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Marc
APPLICANT: GTACKER, Steven
APPLICANT: GTACKER, Steven
APPLICANT: GTACKER, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VEYERION 3.0
SEQ ID NO 25
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PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SEQ ID NO 3057
LENGTH: 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: synthetic construct US-09-761-636A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.0
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202 CLSLPQAPC 210
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US-10-437-963-148570
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Sequence 158427, Application US/10424599

Publication No. US20040031072A1

GENREAL INFORMATION:

APPLICANT: Acvalic David K
APPLICANT: Cao Yongwei

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53223)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 158427

LENGTH: 149
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                                               Score 37; DB 12; Length 94;
Pred. No. 1.1e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_114078C.1.pep
US-10-424-599-158427
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OTHER INFORMATION: unsure at all Xaa locations
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Sequence 3057, Application US/10094749

Publication No. US20030219741A1

GENERAL INFORMATION:
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISHIN, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUNG
APPLICANT: HIC, YURI
APPLICANT: HIC, YURI
APPLICANT: OTSUKA, KERICHI
APPLICANT: TRIE, RYOTARO
APPLICANT: TRIE, RYOTARO
APPLICANT: TRIE, RYOTARO
APPLICANT: MAGHIKO
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                                                         71.2%;
66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                     Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                 1 CISVPLVPC 9
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                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-10-424-599-158427
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US-10-094-749-3057
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(33223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 279501
LENGHER OF THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE CAN THE 
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_48989C.1.pep

US-10-437-963-148570
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OTHER INFORMATION: Clone ID: PAT_MRT3847_94411C.1.pep
US-10-424-599-279501
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 148570
LENGTH: 53
TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|| ::||
13 CLSVLVIPC 21
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ORGANISM: Glycine max
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Search completed: September 5, 2004, 10:29:24 Job time : 26.2727 secs

1: ||||| 28 CMKVPLVP 35

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GenCore version 5.1.6
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               Copyright
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OM protein - protein search, using sw model

Run on:

September 5, 2004, 09:55:30; Search time 8 Seconds (without alignments) 58.079 Million cell updates/sec

US-09-761-636A-14 52 score: Title: Perfect

1 CISVPLVPC Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 seqs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued Patents AA:\* Database

/cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PcTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/pcTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	iland 2 endemons		Semience 6901 An		Sequence 27872. A				48				12,	28	12,	2	169	167	4992.		3. Apr		4 9		4		19, Ap
SOMMERTES	ID	US-08-499-215-5	-341-	-352-6	US-09-341-461-2	60	US-09-489-039A-13375	US-09-252-991A-20960	251-37	US-09-443-184-48	US-09-540-236-2315	US-09-252-991A-23997	US-08-107-684B-11	US-08-609-049A-12	US-08-609-049A-28	US-09-170-996-12	US-09-170-996-28	US-09-461-697-169	US-09-461-697-167	39-543-681A-499	US-09-543-681A-7288	US-07-920-281C-3	US-08-466-277-3	US-09-621-976-4988	-087	US-09-621-976-4028	US-09-252-991A-26531	US-09-544-716-19
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	Score	41	38	38	38	37				35			34			34	34	33	33	33	33	33	m	32.5	32	32	32	32
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Gaps

RESULT 2 US-09-341-461-10 ; Sequence 10, Application US/09341461

75 CASVPLEPC 83

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1 CISVPLVPC

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Sequence 20, Appl Sequence 21, Appl Sequence 11648, A Sequence 11648, A Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 1, Appl Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 3, Appli Sequence 4, Appli Sequence 5, A	3,
US-09-557-921-20 US-09-619-380-21 US-09-489-039A-11648 US-07-988-273-2 US-08-848-810-25 US-09-164-193-21 US-09-221-448A-21 PCT-US93-12019-2 US-09-546-043-5 US-09-546-043-6 US-09-546-043-7 US-09-546-043-7 US-09-546-043-7 US-09-546-043-7 US-09-548-033-7 US-09-548-033-7 US-09-548-031E-4	US-09-546-043-3 US-09-514-885-1 US-08-937-067-7
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### ALIGNMENTS

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Sequence 5, Application US/08499215
Fatent No. 5612204
GENERAL INFORMATION:
FAPLICANT: Saeki, Hisashi
FITLE OF INVENTION: BIOLOGICAL DEGRADATIVE
FITLE OF INVENTION: TREATMENT OF CHLORINE-SUBSTITUTED ETHYLENE
FORRESPONDENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue
CITY: N.W.
STRATE: Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 342;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                          Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.

ZIP: 20037-1202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Versi
SOFTWARE: WOOTBEFFECT version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.8%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.8
Best Local Similarity 77.6
Matches 7; Conservative
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US-08-499-215-5
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Gaps

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GENERAL INFORMATION:
APPLICANT:
:
NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE:
107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27872
LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-489-039A-13375, Application US/09489039A

Sequence 13375, Application US/09489039A

Patent No. 6610816

GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
APPLICANT: CATY BREDONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
FILE REFRENCE: 2709-2004001
FILE REFRENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US-09/489,039A
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US-01-27
PRIOR APPLICATION NUMBER: US-01-29
NUMBER OF SEQ. ID NOS: 14342

SEQ. ID NO 13375
                             , OTHER INFORMATION: amino acid sequence of rat cubilin protein US-09-341-461-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.2%; Score 36; DB 4; Length 455; 66.7%; Pred. No. 2e+02; tive 0; Mismatches 3; Indels
                                                                                                                  Score 38; DB 4; Length 3623;
Pred. No. 7.7e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 4; Length 168;
Pred. No. 51;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27872, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Pseudomonas aeruginosa US-09-252-991A-27872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.2%;
55.6%;
                                                                                                                       Query Match 73.1%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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37 CTSIPGIPC 45
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     US-09-252-991A-27872
       ORGANISM: rat
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Best Local S
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GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION:
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6901
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; Patent No. 6586399
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Verroust, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin TITLE OF INVENTION: and Uses Thereof
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341,461
; CURRENT FILING DATE: 200-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF EQ ID NOS: 40
; SEQ ID NO 2
LENGTH: 3623
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GENERAL INFORMATION:
APPLICANT: Hammond, Timothy G.
APPLICANT: Hammond, Timothy G.
APPLICANT: Verroust, Pierre J.
TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: D6148
CURRENT APPLICATION NUMBER: US/09/341,461
CURRENT FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: PCT/US99/01259
PRIOR APPLICATION NUMBER: PCT/US99/01259
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 10
LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: amino acid sequence of rat cubilin EGF5 repeat US-09-341-461-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 4; Length 44;
Pred. No. 9.2;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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US-09-328-352-6901
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: rat
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US-09-341-461-2
                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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US-09-540-236-2315

Sequence 2315, Application US/09540236

Sequence 2315, Application US/09540236

Sequence 2315, Application US/09540236

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2315

LENGTH: 96
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Patent No. 6551795
GENERAL INFORMATION
ADDITIONATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR RELICATION NUMBER: US 60/074,788
PRIOR RELICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                APPLICANT: Baughn, Mariah
APPLICANT: Baughn, Mariah
APPLICANT: Azimzai, Yalda
APPLICANT: Lall, Preeti
TITLE OF INVENTION NUMBER: US/09/443,184A
CURRENT APPLICATION NUMBER: US/09/443,184A
CURRENT PILLING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 138
SOFTWARE: BERL Program
SEQ ID NO 48
LENGTH: 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1512;
                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 35; DB 4; Length 151
44.4%; Pred. No. 9.8e+02;
tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 96;
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Pred. No. 89;
0; Mismatches
APPLICANT: Seilhammer, Jeffrey J. APPLICANT: Yue, Henry
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87.5%;
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Best Local Similarity 44.4%;
Matches 4; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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1301 CVQVVIIPC 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: M.catarrhalis
US-09-540-236-2315
                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
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                                                Sequence 20960, Application US/09252991A

Sequence 20960, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: ARRUGINGS AND THERAPEUTICS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20960

LENGTH: 90
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57;
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APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Schwaber, James S.
ITILE OF INVENTION: Plant Aminoacyl-tRNA Synthetase;
FILE REPERSING: BB-1193
CURRENT FILING DATE: 1999-07-203
FARLIER PLING DATE: 1999-07-203
FARLIER FILING DATE: July 21, 1998
NUMBER: OF SEQ ID NOS: 37
SOFTWARE: Microsoft Office 97
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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Pred. No.
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GENERAL INFORMATION: APPLICANT: Cunningham, Mary Jane APPLICANT: Zweiger, Gary, APPLICANT: Xeser, Matthew R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 37, Application US/09357251
; Patent No. 6271441
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.0
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1229 CVQVVIIPC 1237
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                                  US-09-252-991A-20960
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US-09-443-184-48
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Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
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848 CVSKPIVVC 856
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GENERAL INFORMATION:
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Patent No. 5552273

GENERAL INFORMATION:
APPLICANT: CLEDIZIAT, Philippe L.
APPLICANT: ROBERT-BAUDOUY, Jeannine
APPLICANT: APALE, Abalo
APPLICANT: GATALL, Jeannine
APPLICANT: GATALL, Jeannine
APPLICANT: GATALL, Jeannine
APPLICANT: GATALL, Jeannine
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                                                                                                                                                                                                                     Length 147;
                                                                                                                                                                                                                 Ouery Match 65.4%; Score 34; DB 4; Length 147
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,684B
FILING DATE: 17-AUG-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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NAME: Berridge, William P.

REGISTRATION UNDRER: 30,024

REFERENCE/DOCKET NUMBER: WPB 28478

TELECOMMUNICATION INFORMATION:

TELEFHONE: (703) 836-2787

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 anino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. BOX 19928
CITY: Alexandria
STATE: VA
                              LENGTH: 147
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                  105 CVSVARPAPAVPC 117
                                                                                                                                                                                                                                                                                                                                                              1 CISV----PLVPC 9
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Best Local Similarity
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                                                                                                                                            US-09-252-991A-23997
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US-08-609-049A-12
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; SEQ ID NO 23997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Gaps
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Sequence 28, Application US/08609049A
Sequence 28, Application US/08609049A
GENERAL INCERNATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Molz, Lisa
APPLICANT: Chen, Yen-Wen
TILLE OF INVENTION:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
APPLICANT: Williams, Lewis T.
APPLICANT: Wolz, Lisa
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 5948664el PI 3-Kinase Polypeptides
CORRESPONDENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 2; Length 1876;
Pred. No. 1.8e+03;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                              COUNTRY: USA

ZIF: 94111-383.4

ZIF: 94111-383.4

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ExtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/609,049A
FILING DATE: 29-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B:
REGISTRAION NUMBER: 29,684
REFRENCE/DOCKET NUMBER: 2307K-063700US
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
TELEPHONE: 1976-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 amino acids
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ZIP: 9411-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC compatible
COMPUTER: IB PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,049A

FILING DATE: 29-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco CTTF: Calfornia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.4%; SCC...
55.6%; Pred. No. ...
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-170-996-12
; Sequence 1.2. Application US/09170996
; Patent No. 6291220
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
APPLICANT: Chen, Yen-Wen
; TITLE OF INVENTION: No. 6291220el PI 3-Kinase Polypeptides
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE SS:
; ADDRESSE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CINY: California
; CONNTRY: USA.
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                                                                                                                                                                                                                                                                                                                     65.4%; Score 34; DB 2; Length 1876; 55.6%; Pred. No. 1.8e+03; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.4%; Score 34; DB 3; Length 1876; Best Local Similarity 55.6%; Pred. No. 1.8e+03; Matches 5; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834

CMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION UNDER: US 08/609,049

FILING DATE: 29-FEB-1996

ATTORNEY/AGENT INFORMATION:
NAME: Dow, KAZEOB E

REGISTRATION NUMBER: 29,684

REFERENCE/DOCKET NUMBER: 2307K-063700US

TELEPHONE: 415-326-2402

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                2307K-063700US
               NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2402
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1876 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.67
Matches 5, Conservative
                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-609-049A-28
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MOLECULE TYPE: protein US-09-170-996-12
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GY: linear
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Qy 1 CISVPLVPC 9

Db 848 CVSKPIVVC 856
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Search completed: September 5, 2004, 10:22:01 Job time : 8 secs

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